

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: December 1, 2003, 08:50:33 / Search time 3972 Seconds  
(without alignments)  
2770.566 Million cell updates/sec

Title: US-10-049-742-11  
Perfect score: 1433  
Sequence: 1 MAGVPEDELNPFHVLGEAT.....VPKGEAKPKRRKKVRRPFOR 269

scoring table: BLOSUM62  
Xgapext 10.0 , Xgapext 0.5  
Ygapext 10.0 , Ygapext 0.5  
Fgapext 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+P2N.model -DEV=x1h  
-O=Cgn2\_1/USPFO\_spool/US10049742/runat\_01122003\_073136\_18605/app\_query.fasta\_1.455  
-DB=GenEmbl  
-QEMT=fastap -SUFFIX=xrge -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=b1s -START=-1 -END=+1 -MATRIX=b1osum62 -TRANS=human40\_cdi -LIST=45  
-DOCALIGN=200 -THR\_MAX=100 -THR\_MIN=0 -MAXLEN=20000000000  
-OUTMT=pho -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL  
-USER=US1049742 @CCNL\_1\_3508 @runat\_01122003\_073136\_18605 -ICPU=3  
-NO\_MMAP -LARGEQUERY -N=3 -SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN -TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

Database :

GenEmbl:  
1: gb\_ba:  
2: gb\_ntg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_dat:  
7: gb\_ph:  
8: gb\_pi:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vl:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pi:  
26: em\_ro:  
27: em\_sts:  
28: em\_un:

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description	
1	1433	100.0	1147	6	AX081438	Ax081438 Sequence	
2	1433	100.0	2343	6	AX713973	AX713973 Sequence	
3	1433	100.0	2343	9	AK055945	Homo sapi	
4	1433	100.0	4274	9	BC050271	Homo sapi	
5	1397	97.5	1818	9	BC016941	Homo sapi	
6	1367	95.4	2402	4	AY027882	Bos tauru	
7	1367	95.4	3159	4	AY027881	AY027881 Bos tauru	
8	1365	95.3	2392	10	AF351783	AF351783 Rattus no	
9	1361	95.0	2694	4	AF308815	AF308815 Bos tauru	
10	1357	94.7	2402	10	BC011146	BC011146 Mus muscu	
11	1306	91.1	2633	11	AC08454	Rattus no	
12	1201	83.8	190201	2	AC129837	Papio anu	
13	1143	79.8	953	9	AF351784	Homo sapi	
14	1112	77.6	747	6	BDD0639	Novel gen	
15	1112	77.6	747	6	BD100577	Novel gen	
16	1051	73.3	754	9	AF141342	Homo sapi	
17	1012.5	70.7	118052	9	AC023055	Homo sapi	
18	1004.5	70.1	247359	2	AC097837	AC097837 Rattus no	
19	777.5	54.3	1253	14	AP268178	AF268178 Bovine vi	
20	766	53.5	1258	14	AF268176	AF268176 Bovine vi	
21	699	48.8	192658	2	AC131081	AC131081 Mus muscu	
22	696.5	48.6	245462	2	AC097931	AC097931 Rattus no	
23	693	48.4	927	14	BDU43603	U43603 Border dise	
24	689.5	48.1	1233	14	AF268172	AF268172 Bovine vi	
25	685	47.8	1004	14	AF268172	AF268172 Bovine vi	
26	618.5	43.2	752	14	AF268177	AF268177 Bovine vi	
27	606	42.3	13203	14	AB078952	AB078952 Bovine vi	
28	601	41.9	13196	14	AB078951	AB078951 Bovine vi	
29	586.5	40.9	873	14	BDU43602	U43602 Border dise	
30	571	39.8	1229	14	AF268180	AF268180 Bovine vi	
31	565	39.4	717	14	BDU42551N1	BDU42551N1	
32	561	39.1	852	14	AF268179	AF268179 Bovine vi	
33	549	38.3	711	14	Z54332	Z54332 Bovine vira	
34	534	37.3	1262	14	AF144617	AF144617 Pestiviru	
c	35	501.5	35.3	211163	2	AC141508	AC141508 Rattus no
36	498	34.8	1145	14	BVDG	BVDG	
37	497	34.7	12119	6	AX057315	AX057315 Sequence	
38	497	34.7	12573	14	M1112	M1112 Bovine vira	
39	497	34.7	12578	14	AJ133738	AJ133738 Bovine vi	
40	497	34.7	12734	6	AR179057	AR179057 Sequence	
41	497	34.7	12734	14	AF2682278	AF2682278 Pestiviru	
42	497	34.7	14078	6	AR123006	AR123006 Sequence	
43	497	34.7	14078	6	AR214645	AR214645 Sequence	
44	497	34.7	14078	6	AR094147	AR094147 Sequence	
45	493.5	34.4	1114	14	AF268175	AF268175 Bovine vi	

#### ALIGNMENTS



HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.									
Db	782	AGCGGGTCAAGTAATGAGITCTGTCCAACCTGAGATACCTCAAGGGCAATGAA	841						
Qy	101	ThrMetMetCysSerArgCysGlnGlyLysHisArgArgPheGluMetAspArgGluPro	120						
Db	842	ACTATGATGTGATGCCATCAAGAACCATAGGGTTGAAATGGACCGGAAACCT	901						
Qy	121	LysseriaAlaArgTyrTysCysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspHe	140						
Db	902	AAGACTGGCAGATACTGTGGTAACTGGCTGCATCTGTGAGGAAGGGACTT	961						
Qy	141	TrpAlaGluSerSerMetLeuGlyLeuLyslethrtryrheAlaLeuMetAspLeuLys	160						
Db	962	TGGCAGAGCCAAAGATGTTGGGCTCAAGATCACCTACTTGACTGTGGTGAAG	1021						
Qy	161	ValtyrAspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHis	180						
Db	1022	GTTATGACATCACAGAGTGGCTGATGCCAGATCCCCAGATACCCAC	1081						
Qy	181	ArgValProTyrrHisIleSerPheGlySerArgIleProGlyThrArgGlyArgGlnArg	200						
Db	1082	AGAGTCCCCTATCACATCATTGTTCTCGGATTCAGGCCACCAAGGGCCAGAGA	1141						
Qy	201	AlaThrProAspAlaProProAlaAspLeuSerArgIlePheGlnVal	220						
Db	1142	GCCACCCCAATGCCATGCCCTCTGGTGTCTAGATTCTGAGTGGATCTTCAGTA	1201						
Qy	221	ProProGlyGlnMetProAsnGlyAsnPheHeAlaAlaProGlnProAlaAla	240						
Db	1202	CCCCAGGGAGATGCCCAATGGAAACTTTCAGCTCTGAGTCCTCAGCCCTCGAGCC	1261						
Qy	241	AlaIlaAlaSerLysProIhsSerThrValProLysGlyGluAlaLysPhePolyAspArgArg	260						
Db	1262	GCTSCAGCCTTAAGCCCAACGACAAGTACGAACTCCAGGGAGAAAGCCAAACCTAACGGCCGG	1321						
Qy	261	LysLysvalArgArgProPheGlnArg	269						
Db	1322	AAGAAAGTGGAGGCCCTTCAGT	1348						
RESULT 3									
Ak05945	Ak05945	AK05945	2343 bp	tRNA	PRI 01-AUG-2002				
LOCUS		Homo sapiens cDNA FLJ31382_fis							
DEFINITION		Hom sapiens cDNA FLJ31382 fis, clone NINPC200206, highly similar to Bovine viral diarrhea virus type 2 strain BVDV2-SD1630C polyprotein gene.							
ACCESSION	Ak05945								
VERSION	Ak05945.1	GI:16550797							
KEYWORDS		Oligo capping; fis (full insert sequence).							
SOURCE	Homo sapiens (human)								
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1	Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Furukawa, Y., Fujimoto, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsubo, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakanura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kaneshori, K., Takahashi, Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagai, K., Nagai, Y., Nagai, X. and Isogai, T.							
TITLE	NEDO human cDNA sequencing project								
AUTHORS	Isogai, T., Otsubo, T. and Sugiyama, T.								
JOURNAL	Direct Submission								
REFERENCE	Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp), Tel: +81-438-52-3975, Fax: +81-438-52-3966								
AUTHORS	902	AAGACTGGCAGATACTGTGTCAGATAGGTGAATAGGTGCAATCTGAGGAGGACCTT	961						
JOURNAL	141	TrpAlaGluSerMetLeuGlyLeuLysIleThrPheAlaLeuMetAspGlyLys	160						
COMMENT	NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) supported by Japan, RAB Technology Center etc.)								
AUTHORS	962	TGGCGAGTCAGCTAACGATGTTGAGCTTCAAGATCACCTACTTGCATGATGGAAAG	1021						
JOURNAL	161	ValTyrAspIleThrGluTrpAlaGlyCysGluArgValGlyIleSerProAspThrHis	180						

Db	1022	GTCATGAACTACAGAGTGGGCTGATGCCAGGGTAGGTATCCCAGATCCAC 1081
Qy	181	ArgValProlTyrosIleSerPheClySerArgIleProGlyThrArgGlyArgIleGlyArg 200
Db	1082	AGAGCCCTATCATCATCTATGGTTCTCGATTCCAGCACAGGGCAGAGAGA 1141
Qy	201	AlaThrProAspAlaProProAspLeuGlnAspPhLeuSerArgIlePheGlnVal 220
Db	1142	GCCACCCAGATGCCCTCTGCATCTCAGATTCTCTGACTGGATCTTCAGATA 1201
Qy	221	ProProGlyIleMetProAsnGlyAsnPheAlaAlaProGlnProAlaProGlyAla 240
Db	1202	CCCCAGGCGAGTCCCCATGGGAACCTCTGGCTCTAACCTGAGCTGGCC 1261
Qy	241	AlaAlaAlaSerIleProAsnSerThrValProLysGlyGluAlaLysProLysArgArg 260
Db	1262	GCTGAGCCCTCAKCCCAAACAGCACAGTACGACCAAGGGAGAAAGCCAAA CCTAAACGGCCG 1321
Qy	261	LysLysValArgIleArgProPheGlnArg 269
Db	1322	AAGAAAGTGAGGGGGCCCTTCCAAAGT 1348
RESULT 4		
LOCUS	BC050271	4274 bp mRNA linear PRI 11-APR-2003
DEFINITION	Homo sapiens	Similar to RIKEN CDNA 5730551F12 gene, clone MGC:17391 IMAGE:3913714, mRNA, complete cds.
ACCESSION	BC050271	
VERSION	BC050271.1	GI:29792138
KEYWORDS	MGC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 4274)
AUTHORS	Strauberg, R.	
TITLE	Direct Submission.	
JOURNAL	Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
COMMENT	Contact: MGC help desk Email: cgabbs-1@mail.nih.gov	
Tissue	Procurement: ATCC	
CDNA Library Preparation:	Life Technologies, Inc.	
Arrayed by:	The I.M.A.G.E. Consortium (LILN)	
DNA Sequencing by:	Sequencing Group at The Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305	
Web site:	<a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a>	
Contact:	(Dickson, Mark) mcd@paxil.stanford.edu	
Dickson, M., Schmitz, J., Grimes, J., Rodriguez, A., and Myers, R. M.		
FEATURES		
source	1. .4274	/organism="Homo sapiens"
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RESULT 5

Db 2052 CCCCAAGGGCAGTGCCTGAGCTCCGCCCTGGAGCC 2111 Alignment Scores: 7.57e-89 Length: 1818  
Pred. No.: 139.00 Matches: 262  
Score: 139.00% Conservative: 1  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 99.62% Indels: 0  
Query Match: 97.49% Gaps: 0  
DB: 9 US-10-049-742-11 (1-269) x BC016941 (1-1818)

Qy 1 Met Ile Glu Val Pro Glu Asp Glu Leu Asn Pro Phe His Val Ile Glu Val Glu Ala Thr 20  
Db 188 ATGCCTGGGTTCTGGATGAGCTAACCTTCCTGATCTGGGGTTAGGCCAA 247  
Qy 21 Alas er Asp Val Glu Leu Lys Alanine Arg Glu Leu Ala Val Met Val His Pro Asp 40  
Db 248 GCATCAGATGTTGAACTAAGAGGCCATAGACGCTGGACTGATGGTCATCCGTGAC 307  
Qy 41 Lys Asn His Pro Arg Glu Arg Glu Glu Lys Alanine Arg Glu Leu Ala Glu Asn Glu Leu 60  
Db 308 AAAATCATCATCCCCGGCTGAGGCCCTCAAGGTTTGGAGCAGCTGGAGATT 367  
Qy 61 Val Ser Asn Ala Glu Lys Arg Lys Glutyr Glutamyl Asp Met Ala Glu Asn Glu Leu 80  
Db 368 GTGCAATGCTAAAAGGAGTAGATGAGTAAGAAGCTGGAGAGATGACCTG 427  
Qy 81 Ser Arg Ser Val Asn Glu Phe Leu Ser Lys Leu Glu Lys Asp Leu Lys Glu Ala Met Asn 100  
Db 428 AGCGGGTAGTAAATGACTTCTGTCRAAGTCGAACATGACCTCAAGGGCAATAAT 487  
Qy 101 Thre t Met Cys Ser Arg Cys Gln Gln Lys Arg Lys His Pro Ala Glu Glu Lys Asn Arg Pro Asp Arg Pro 120  
Db 488 ACTATGATGTCAGCCATGCCATGGCAAGGAAAGCATTGGACCGGAACCT 547  
Qy 121 Lys Ser Ala Arg Tyr Cys Ala Glu Cys Asn Arg Leu His Pro Ala Glu Glu Lys Asn Arg Pro Asp Arg Pro 140  
Db 548 AAATGGCCAGATCTGCTGAGCTGATAGGTGAACTGGGAAACGAGACTT 607  
Qy 141 Tryptalaglu User Ser Met Leu Gly Leu Lys Ile Thri Ty Phe Ala Leu Met Asp Gly Lys 160  
Db 608 TGGCAGGGTCAGCACTGCTGGCCCTAAAGTCACCTACTTGCACTGATGGATGAAAG 667  
Qy 161 Val try Asp Ile Thr Glu Trp Alan Gly Cys Gln Arg Val Gly Ile Ser Pro Asp Thr His 180  
Db 668 GTCATGACATCACAGTGTGGCTGATGGCTGATGGCTGATGGATACCCAC 727  
Qy 181 Arg Val Pro Ty Rhi S11 Ile Ser Phe Gly Ser Arg Ile Pro Gly Thr Arg Glu Arg Glu Arg 200  
Db 728 AGAGTCCCCTATCACATCTCATTTGGGTTCTGGATTCAGGACACAGGGCCGAGAGA 787  
Qy 201 Ala Thr Pro Asp Ile Pro Pro Ile Asp Leu Ser Arg Ile Pro Gly Thr Arg Glu Arg Glu Arg 220  
Db 788 GCCACCCAGATGCCCTCCCTGCTGATCTGAGATTCTGAGTCATCTTCAGTA 847  
Qy 221 Pro Pro Gly Glu Met Pro Asn Gly Asn Phe Phe Ala Ala Pro Glu Pro Ala Pro Gly Ala 240  
Db 848 CCCCAAGGGCAGATGCCCAATGGAAACTCTTGCAGCTCCCTCAGCCTGCCCTGAGGCC 907  
Qy 241 Ala Ala Ala Ser Lys Pro Asn Ser Thr Val Pro Lyg Gly Glu Ala Iys Pro Lys Arg 260  
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AYLEEHAEEEANEEDVIGDEEEETPKPIEVPKEEPPEPTDVAAEKVVKITSEI  
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FEATURES

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POTERKQRAFENPVNSPLESKKVARAFGSSPKLGSAAKCFMVNDLKLKERAQ  
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RESULT 6

LOCUS AY027882 2402 bp mRNA DEFINITION Bos taurus J-domain protein Jiv mRNA linear  
ACCESSION AY027882 VERSION AY027882.1 GI:15777194 KEYWORDS

BASE COUNT 532 a 373 c 494 g 419 t

ORIGIN

SOURCE	Bos taurus (cow)	Db	1610 AAAATCATCATCTCGTCGAGCTTCAGGTTTGGGAGCTGGGATT 1669
ORGANISM	Bos taurus	Qy	61 ValSerAsnAlaGluLysBarglyGluMetArgMetAlaGluAsnGluLeu 80
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
Bovidae; Bovinae; Bos.	1 (bases 1 to 2402)	1670 GTCGCCAACCCAAAGGGAGAATGAGTGAACGATGGAGAAATGACTG 1729	
REFERENCE	Rinck, G., Birghan, C., Harada, T., Meyers, G., Thiel, H.J. and Tautz, N.	Qy	81 SerArgSerAlaGluLysLeuAspAspLeuLysGluAlaAsn 100
A cellular J-domain protein modulates polyprotein processing and			
cryptic antigenicity of a pestivirus		-----	-----
J. Virol. 75 (19), 9470-9482 (2001)	11533209	1730 AGCGGTCACTGATGAGTTCTCAGTGCAA ----- 1777	
AUTHORS	Rinck, G., and Tautz, N.	Qy	101 ThrMetMetCysSerAlaGluLysGlnGlyLeuAspArgGluPro 120
TITLE	Direct Submission	Db	1778 ACGTGTCTGCAGCGATGCCGAAAGCATGGGGAGCACT 1837
JOURNAL	Submitted (22-FEB-2001) Institut fuer Virologie (FB10),	Qy	121 LysSerAlaArgTyrcysAlaGluCysAsnArgLeuHisProAlaGluGlyAspHe 140
MEDLINE	Justus-Liebig-Universitaet Giessen, Frankfurterstrasse 107, Giessen	Db	1838 AAGGTGCCAGATACTGCTGAGTAATGCTGATCTGTAAGGAACTGACTT 1897
REFERENCE	2 (bases 1 to 2402)	Qy	141 TrpAlaGluSerSerMetLeuGlyLeuLysIleThrPheAlaLeuMetAspGlyLys 160
AUTHORS	Rinck, G., and Tautz, N.	Db	1898 TGGCAGACTCAACCATACTGTTGGCCTCAAATCACCTACTTGCCTGATGGAAAG 1957
TITLE	Direct Submission	Qy	161 ValTyrAspLethrGluTrpAlaGlyLeuLysIleThrPheAlaLeuMetAspGlyLys 180
JOURNAL	Submitted (22-FEB-2001) Institut fuer Virologie (FB10),	Db	1958 GTGTATGATATCACAGTGGCTGGATCTCCCAAGATACCCAC 2017
FEATURES	Location/Qualifiers	Qy	181 ArgValProTyroRhisIleSerPheGlySerArgIleProGlyThrArgGlnArg 200
source	1. .2402	Db	2018 AGAGTCCCTTATCACATCTCATTCAGTGGCAGCACAGTGGCCAGAGA 2077
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/cell_line="MBBk"		Db	221 ProProGlyGlnMetProAsnGlyAsnProhePheAlaAlaProGlnProGlyAla 240
/codon_start=1		Qy	2138 CCCAGGGCAGATGTCACAGGAACTCTTGCCTCCAGTCGGCCCTGGGCC 2197
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/translation="MAKRFEGGLCGAHSSGASLRITLGPSPVDPDILSFGLRDSAG		Qy	261 LysLysvalArgArgProProGlyGlnArg 269
SAPNPTRCRTHSSPKYTOPNPNAHMSPSKTCAGGSPRGPGLAEDPDOSAESEESGV		Db	2258 AGGAAGTGGAGGGCCCTTCCAAACGT 2284
DOBLSRENEFGYODGNSSPLSISIPTSTCNCGGAACTTCAGGAACTCTTGCCTCCAGTCGGCCCTGGGCC 2197		RESULT?7	
ALGDEDEBEYDEDEPLKPSDPSDVPSPSKKAPPRQRHRVPAKDRGGERDPRS		AY027881	
PGRHLGRKESQADERRGRLGQAFWNLLEVLVGEVETCGHLLY		LOCUS	AY027881 3159 bp mRNA linear NAM 25-SEP-2001
CROKGSDDUILLRVMVNGWMLGRQWMAQWQFOUSGFCYGAISLTFRULVGALLIY		DEFINITION	Bos taurus J-domain protein JIV mRNA, complete cds.
ALALLLGCLQMLQMLRVLGLSLRGLWDKATNTFWSWASPTQRCILILRSREWQQLV		ACCESSION	AY027881
RIVONGWLEPPWKRONTRNAAPAGGRYCPPEEVARLTINAGVPEDELNPFHVLG		VERSION	AY027881.1 GI:15777192
MAENELRSRNFEFLSKQEMANTMCSRCGKHFENDREPKSARTCAENCRNLHAE		KEYWORDS	
EGDFWAESSMLGKITYFAMLDKVYDITWAGORVGSIDTRVPHISFSRMPG		SOURCE	Bos taurus (cow)
TSGRCRATPAPPADLQDFLSRIFQVPPGOMSNFGFAAPQPQPGATAASKNSTVPK		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
GEAKPCKRKVKRPQR"		DB_TAXON	Mammalia; Bovidae; Cervidae; Ruminantia; Pecora; Bovidae;
3' UTR	2288 .2282	note="use of alternative polyadenylation site results in	Bovidae; Bovine; Bos.
		3' UTR shorter than in the sequence presented in GenBank	1 (bases 1 to 3159)
BASE COUNT	559 a	Accession Number AY027881	Rinck, G., Birghan, C., Harada, T., Meyers, G., Thiel, H.J. and Tautz, N.
ORIGIN	582 c	527 t	. A cellular J-domain protein modulates polyprotein processing and
			cytopathogenicity of a pestivirus
			J. Virol. 75 (19), 9470-9482 (2001)
			JOURNAL
			2 (bases 1 to 3159)
			21424330
			11533209
			REFERENCE
			Rinck, G., Birghan, C., Harada, T., Meyers, G., Thiel, H.J. and Tautz, N.
			. Authors
			Direct Submission
			Submitted (20-FEB-2001) Institut fuer Virologie (FB10),
			Justus-Liebig-Universitaet Giessen, Frankfurterstrasse 107, Giessen
			35392, Germany
			FEATURES
			Location/Qualifiers
			1 . 3159



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Db	1997 CGAGTCCTTACCAATCTCATTCCTTCCTGTCAGGTGACCTGGGATCTTCAAGTA	2056				
Qy	221 ProProGlyGlnMetProAsnGlyAsnProPheAlaAlaProGlyAla	240				
Db	2117 CCTCAGGGGATGTCACATGGGACTCTTGGCACTCCACCTGGCCCTGGGACT	2176				
Qy	241 AlaAlaAlaSerLysProAsnSerThrValProlysGlyGluAlaLysProLysArgArg	260				
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Qy	261 LysLysValArgProProGlyAla	269				

Qy	A	P	COMMENT	
21	AlaseraspvalGlueulyslysAlatyrArgGlnLeuAlavaImetvalIhisProAsp	40	Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center: Center code: BCM-HGSC	
Db	1245	GCATCAGATGTGAACCTGAAAGGCTATGGCACTGGAGTGTATCTTGAC	1304	Web site: http://www.hgsc.bcm.edu/cdna/
Qy	41	LYSASPDIHISproArgAlaGluGluAlaPheLysValleuArgAlaAlaItrPaspIle	60	Contact: amg@bcm.tmc.edu
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Qy	61	ValSerAspAlaGluLysArgLysGluMetLysArgMetAlaGluAsnGluLeu	80	This Clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan Gene Prediction.
Db	1365	GTCAGGAAACCCTGAAAGCCGAGGAAATATGAGATAACCAATGAGCTG	1424	Location/Qualifiers
Qy	81	SerArgSerValAsnGluPheLeuSerLysLeuGlnAspAspLeuLysGluAlaMetAsn	100	1. .2402 /organism="Mus musculus" /mol_type="mRNA" /strain="CZECH II" /db_xref="taxon:10090" /clone="MGC:19282 IMAGE:4016209"
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Qy	121	LysSerAlaAlaGlyTyrCysAlaGluCysAsnArgLeuHisProAlaGluGluLysAspPhe	140	BASE COUNT
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Qy	141	TrpAlaGluSerSerMetLeuGlyLeuIleThrTyPheAlaLeuMetAspGlyLys	160	ORIGIN
Db	1593	TGGCACAGTAGCAGATGTTGGCCTCAAATCACCTACTTGCTGTGATGAAAG	1652	US-10-049-742-11 (1-269) x BC011146 (1-2402)
Qy	161	ValTyPaspIleThrGluItpDalaGlyCysGlnArgAlaGlyIleSerProAspThrHis	180	Alignment Scores:
Db	1653	GTGTATGATATCACAGGGCCCTGGAAATCTCCCAGATACCCAC	1712	Score: 6.551e-86
Qy	181	ArgValProTyRHisIleSerPheGlySerArgIleProGlyThrArgLyArgGlnArg	200	Length: 2402
Db	1713	AGAGTCCCTTATCACATCTCATTTGGTTCAGGATGCCAGCACAGTGGCAAGGA	1772	Matches: 1357/00
Qy	201	AlaThrProAspAlaProProAlaAspLeuGlnAspPheLeuSerArgIlePheGlnVal	220	Percent Similarity: 95.91%
Db	1773	GCTACTCGAGTCAGGCCCTCCGCTGACCTTCAGGATTCTTGAGCCGATTTCAAGTA	1832	Best Local Similarity: 92.9%
Qy	221	ProProGlyGlnMetProAspGlyIyanPheHeAlAlaProGlnProAlaProGlyAla	240	Query Match: 94.70%
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Qy	241	AlaAlaAlaLysProAsnSerThrValProLyGluIalAlaProLySArgArg	260	Mismatches: 11
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ACCESSION	5710551F12	clone MG:19282		
VERSION	4016209	mRNA, complete cds.		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REMARK				

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 LOCUS Rattus norvegicus clone CH230-2H10, WORKING DRAFT SEQUENCE, 3  
 DEFINITION unordered pieces.

ACCESSION AC098454  
 VERSION HTG - HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Rattus.  
 REFERENCE 1 (bases 1 to 263371)  
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
 Alisbrooks,S.L., Amaralutunge,H.C., Are,J.R., Ayale,M., Banks,T.,  
 Barbaria,J., Benton,J., Bingham,K., Blankenburg,K., Bonnin,D.,  
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
 Buhay,C., Burch,P., Burkett,C., Carter,M., Carazos,S.R., Chacko,J., Chavez,D.,  
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
 Delaney,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Farnhart,C., Edgar,D., Edwards,C.C., Elhai,C., Escott,M.,' Escott,M.,' Frantz,P.,  
 Faust,T., Ferraguto,D., Flagg,N., Ford,J., Fosier,P., Gall, R.,  
 Gabisi,A., Gao,J., Garcia,T., Garner,T., Garza,N., Hale,S., Hamilton,K.,  
 Gorrell,J.H., Guerevara,W., Gunaratne,P., Hart,M., Hawes,A., Hernandez,J.,  
 Harris,C., Harris,K., Hart,M., Havlat,P., Hawes,A., Hernandez,J.,  
 Hernandez,O., Hodges,A., Hogue,M., Holloway,C., Hollins,B.,  
 Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
 Jacobson,B., Jia,Y., Johnson,K., Joly-Let S., Joudah,S.,  
 Jacobson,B., Jia,Y., Johnson,K., Joly-Let S., Joudah,S.,  
 Karlovic,J., Kureishi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,  
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 Massey,E., Mawhinney,B., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,  
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 Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,  
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 Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S.,  
 Usmani,K., Vasquez,L., Vera,V., Warren,R., Washington,C., Watlington,Q.,  
 Wang,S., Ward-Moore,S., Williamson,A., Wleczky,R., Woodens,S., Worley,K.,  
 Wu,C., Wu,Y., Wu,Y.P., Zhou,J., Zorrilla,S., Nelson,D.,  
 Weinstock,G., and Gibbs,R.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 263371)  
 AUTHORS Worley,K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 REFERENCE 3 (bases 1 to 263371)  
 AUTHORS Worley,K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-OCT-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT On Oct 10, 2002 this sequence replaced gi:21953452.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a "contig-scaffold"). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: TUD  
 Center clone name: CH230-2H10  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 243674 bases at least Q40  
 Consensus quality: 246830 bases at least Q30  
 Consensus quality: 248548 bases at least Q20  
 Estimated insert size: 247731; sum-of-contigs estimation  
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.edu/docs/Genbank_draft_data.html)).  
**NOTE:** This is a 'worrying draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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1. 1190201

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ORIGIN

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Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-049-742-11 (1-269) × AC129837 (1-190201)

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Qy 41 LysAsnHiShisProArgAlaGluAlaPhoLysValLeuArgAlaAlaAlaAlaAspAla 60

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Qy 61 ValSerAsnAlaGluIysArgLysGluItyGluMetLysArgMetAlaGluAsnGluLeu 80

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Qy 101 ThrMeMetCysSerArgCysGlnGlyLysHiSargArgPheGluMetAspArgGluPro 120

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Qy 121 LysSerAlaArgTyrcysAlaGluCysAspArgLeuHisProAlaGluGluGlyAsphe 140

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Qy 201 AlanineProAspAlaProProAspLeuSerArgLysPheGlnVal 220

Db 118438 GCCACCGGCAAGCAGCCCTCCCTGGCTGATCTCAGGTTCTGAGTCAGATCTTCAGTA 118497

Qy 221 ProProGlyGinMetProAsnSerPheGlySerArgLysPheAlaAlaProGlyAla 240

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Qy 241 AlaAlaAlaSerLysProAsnSerThrValProlysGlyGluAlaIysProlysArgArg 260

Db 118558 ACTGGCAAGCTTAAAGCCCAACGGCAAGTACCCAAAGGAGAAACCAACGAA 118617

Qy 261 LysLysValArgArgProphGlnArg 269

Db 118618 ACGAAAGTGAGGGGCCCTCCAAACGGT 118644

RESULT 1.3

AF351784

LOCUS AF351784

DEFINITION Homo sapiens dopamine receptor interacting protein mRNA, partial cds.

ACCESSION AF351784

VERSION AF351784.1

KEYWORDS

ORGANISM

Homo sapiens (human)

Bukreyeva, M.

Chordata: Craniata: Vertebrata: Euteleostomi:

Mammalia: Butheria: Primates: Catarrhini: Hominoidea: Homo.

REFERENCE 1 (bases 1 to 953)

AUTHORS Bernak, J.C., Li, M., Bullock, C. and Zhou, Q.-Y.

TITLE Regulation of transport of the dopamine D<sub>1</sub> receptor by a new membrane-associated ER protein

JOURNAL Nat. Cell Biol. 3 (5), 492-498 (2001)

MEDLINE 2123.1.75

SUBMED 11331877

2 (bases 1 to 953)

AUTHORS Bernak, J.C., Li, M., Bullock, C.M. and Zhou, Q.-Y.

TITLE Direct Submission

JOURNAL Submitted (21 FEB 2001). Pharmacology, University of California, Irvine Blvd., Irvine, CA 92697, USA

FEATURES Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No. :

2.11e-71

Length: 953

Matches: 213

Score: 1143.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 79.76%

DB: 9

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Origin:

US-10-049-742-11 (1-269) × AF351784 (1-953)

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Qy	157	MetAspGlyLysValTyrAspPleIleThrGluLysPheAlaGlyGlyIleSer	176	Qy	35	ValMetValHisProAspLysSerAsnHisSerProArgNlaGluGluAlaLpheLysValLeu	54
Db	303	ATGATGAAAGGTATGACATCACAGTGGCTGATGCCAGCTGTAAGTCTCC	362	Db	96	GATGATGGTCATCTGCAAAATCATATCCCGGCTGAGGGCTCAAGGTTTG	155
Qy	177	ProAspThrHisArgValProtryptHistIleSerAspGlySerArgIleProGlyThrArg	196	Qy	55	ArgAlaAlaLpheAspIleValSerAsnAlaGluLysBargLysGluLysGluMetLysArg	74
Db	363	CCAGATACCAACAGTCAGTCCTATCACATCATTGGTTCTGGATTCAGGCCACAGA	422	Db	156	CGGCAAGTTGGCACATGTCAAGCAATGCTGCAAGCTGCAAGATGAAACGA	215
Qy	197	GlyArgGlnArgAlaThrProAspAlaProAspPheAlaAlaProGlnPro	216	Qy	75	MetalGluAsnGluLpheUserArgSerValAsnGluPheLeuSerLysLeuGlnAspAsp	94
Db	423	GGGGGCGAGAGCGCACCCAGATGCCCTCCGCTGATCTAGGATTCTGAGTCGG	482	Db	216	ATGCGAGAAATGAGCTAGCCGGTCAGCTGCAAGCTGCAAGATGAC	275
Qy	217	IlePheGlnValProProGlyGlnMetProAsnGlyAspPheAlaAlaProGlnPro	236	Qy	95	LeuLysGluAlaMetAsnThrMetMetCysSerArgIleSerGlyLysLysBargLysArgPhe	114
Db	483	ATCPTTCAGTACGGTACCCCCAGATGCCAACTCTTGCAGCTCCCTCAGCT	542	Db	276	CTAACAGGCCAATGAATACTATGATGATGTCAGCGATGCCAAAGGAACTGGGTT	335
Qy	237	AlaProGlyAlaAlaAlaAlaSerLysProAsnSerThrValProLysGlyGluAlaLys	256	Qy	115	GluMetAspArgGluProLysSerAlaArgArgTycSylAlaGluCysAsnArgLysHisPro	134
Db	543	GCCCCCTGGGACCCGGCTGCAAGCTCTAAGCCAAACAGCACAGTACCAAGGAAAGCCAA	602	Db	336	GAATGGACCGGGAACTTAAGATGTCAGTGGCAGATATGGCTCCATCTCT	395
Qy	257	ProLysArgArgLysLysValAlaArgArgProPheGlnArg	269	Qy	135	AlaLysGluGlyAspPheTrpAlaGluUserSerMetLeuGlyLeuLysIleThrPhe	154
Db	603	CCTAACGGGGAAAGAATGAGGGCCCTTCCAACAGT	641	Db	396	GCTGAAGGAGGAGCTTGGCAGAGTAAAGCATGTTGGCTCAAGATCACCTACTT	455
RESULT	14	B0020639	B0020639	Qy	155	AlaLauMetAspGlyLysValTyAspIleThrGluLrpAlaGlyCysGln-ArgAlG	174
LOCUS	DEFINITION	Novel gene and novel gene fragment cloned in human neuroblastoma.	Db	456	GCACTGATGGATGGAAAGGTGTAGACATCACAGAGTCGCTGATGCCGCTGAG	515	
ACCESSION	VERSION	B0020639	GI:22561815	Qy	174	YlleserProAspThrHisArgValProtryptHistIleSerPheGlySerArgLysProG	194
KEYWORDS	SOURCE	B0020639..1	JP2001245671-A/2877	Db	516	TATCICCCAGATAACCACAGTCCTCATCTCATCTATTTGTTGGATTCAGGTCAGG	575
ORGANISM	Homo sapiens	(human)	Homo sapiens	Qy	194	YthrArgGlyArgGlnArgAlaThrProAspAlaProProAlaSpLeuGlnAspPhe	214
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 747)	Db	576	CACCAAGGGGGAGAGGCCACCCAGATGCCAGAGTGCCTCTGCTGATCTCAGGATTCT	635	
REFERENCE	AUTHORS	AKAGAWARA, A.	Qy	214	uSerArgGlyIlePheGlnValProProGlyGlnMetProAsnGlyAnPheAspAlaAlaPr	234	
TITLE	JOURNAL	Novel gene and novel gene fragment cloned in human neuroblastoma	Db	636	GAGTCGAATCTTCAGTACCCAGGCANATGCCAATGGAACTTCCTTGACCTTC	695	
PATENT	OS	Patent: JP 2001245671-A/2877	Qy	234	oGlnProAlaSpProGlyAlaAlaAlaAlaLysProAsnSerThrValProLys	252	
COMMENT	PI	CHIBA PREF, HISAMITSU PHARMACEUTICAL CO INC	Db	696	6AA-TAA-CCCTGGCCCTGGCCCCGTTGAAACNTNTAAGG--CAACAGNAACATACCAAG	746	
PD	07-MAR-2000	JP 20000159195	RESULT	15	747 bp DNA linear	PAT 27-AUG-2002	
PC	07-MAR-2000	AKIRA NAKAGAWARA	LOCUS	BD100577	Novel genes cloned in human neuroblastoma and fragments thereof.		
PC	07-MAR-2000	PI	DEFINITION	BD100577	Novel genes cloned in human neuroblastoma		
CC	07-MAR-2000	PI	ACCESSION	BD100577	Novel genes cloned in human neuroblastoma		
CC	07-MAR-2000	PI	VERSION	BD100577..1	Novel genes cloned in human neuroblastoma		
FEATURES	FT	Location/Qualifiers	KEYWORDS	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
FEATURES	FT	Location/Qualifiers	SOURCE	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
FEATURES	FT	Location/Qualifiers	ORGANISM	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
BASE COUNT	source	1..747	COMMENT	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
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ORIGIN	200 g	165 t	COMMENT	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
			COMMENT	WO 0166719-A/2877	Novel genes cloned in human neuroblastoma		
Alignment Scores:	Pred. No.:	2.36e-69	Length:	747			
Score:		1112.00	Matches:	216			
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Best Local Similarity:		90.38%	Mismatches:	19			
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DB:		6	Gaps:	1			
US-10-049-742-11 (1-269) x BD020539 (1-747)	Qy	15 LenglyvalGluAlaSerAspValGluLeuLysAlaTyrArgGlnLeuAla	34	FT	1 . 747		

FEATURES FT Location/Qualifiers  
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1. 747  
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BASE COUNT 191 a 167 c 200 g 165 t 24 others

ORIGIN 1 24 others

Alignment Scores:

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US-10-049-742-11 (1-269) × BD100577 (1-747)

Qy 15 LeucylvalGlualathAlaSerAspValGluLeuLysAlaTyrArgGlnLeuAla 34  
Db 36 TGGGCATGTTGCGCTACTGGAGAGCTTGAACTGAAAGCCATAGAACGTCGCA 95

Qy 35 ValMetValHisProAspLysAsnHisHisProArgAlaGluGluAlaPheLysValLeu 54  
Db 96 GTGATGGTTCATCCTGACAAAAATCATCATCCTCCGGCTGAGGGCTTCAGGTTTG 155

Qy 55 ArgAlaAlaAlaTrpAspLysValSerAlaSerAlaGluLysAlaGlyLysLutYGLutMetLysAla 74  
Db 156 CGGAGCGCTGGCACATCTGCAATGCTGAAAGGCCAAGAGTATGAGTAACGA 215

Qy 75 MetAlaGluAsnGluLeuSerArgSerValAsnGluPheLeuSerLysIleuGinAspAsp 94  
Db 216 ATGGCAGAAATGAGCTGGCGCTAGAAATGAGTTCTGTGCAAGTCAGAAGTGC 275

Qy 95 LeuLysGluAlaMetAsnThrMetCysSerArgCysGlnLysLysIleuArgArgPhe 114  
Db 276 CTCAGGGAGCCAATGAATCATGATGTCAGTGTAGCCGATGCCAAAGAACTAGAGGTT 335

Qy 115 GluMetAspArgGluProLysSerAlaArgTyrcysAlaGluCysAspArgLeuHisPro 134  
Db 336 GAATGGACGGGAACCTAGATGTCAGTGTCCAGATACTGTGCTCAGTGTAAATGGCTGCACTT 395

Qy 135 AlaGluGluGlyAspPheTrpAlaGluSerSerMetLeuGlyLeuLysIleuThrTyrPhe 154  
Db 396 GCTAGGGAGGAGCTTTGGCAAGACTAACATGTTGGCTCAAGATCACCTACTTT 455

Qy 155 AlaLeuMetAspGlyLysValtyrAspIleThrGluIlePheLysAlaGln-ArgValGln 174  
Db 456 GCACTGATGATGGAAAGGTGATGACATCACAGTGGCTGATGCCAGCGTGTAG 515

Qy 174 YIleSerProAspThrHisArgValProThrHisIleSerProGlySerArgIleProGln 194  
Db 516 TATCTCCCAAGATAACCAAGATGCCATCATCTATTGTTCTGGATTCCAGG 575

Qy 194 YThrArgGlyArgGlnArgAlaIleProAspAlaProProAlaAspLeuGlnAspPheLe 214  
Db 576 CACCAAGGGCGGGAGAGGCCACCCAGATGCCCTTCGCTGATCTCAGATTCTCT 635

Qy 214 uSerArgIlePheGlnValProProGlyGlnMetProAsnGlyAsnPheAlaAlaAlaPhe 234  
Db 636 GAGTCGAATCTTCAGTACCCAGGGCANATGCCATGGGACTTCTTGOAGCTTC 695

Qy 234 oGinProAlaProGlyAlaAlaAlaAlaSerLysProAsnSerThrValProlys 252  
Db 696 TAA-CCTTCCCCTGGACCCGGTGAACNTAAGC---CAACAGNACATPACCCAG 746

Search completed: December 1, 2003, 11:25:05

Job time : 41.69 secs

SUMMARIES										
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3	1430	99	8	3286	24	AAI9602				
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5	1051	73	3	754	24	ABX0184				
6	1051	73	3	754	24	ABST7460				
7	1051	73	3	754	24	AAS3081				
8	1012.5	70	7	7453	22	AAL06261				
9	1012.5	70	7	7453	22	AAC86336				
10	497	34	7	12119	22	AAC86336				
11	497	34	7	12578	21	AAZ36196				
12	497	34	7	12734	24	ABA9515				
13	497	34	7	12842	21	AAZ36103				
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C	25	195.5	13	1030	22	AAS27153				
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C	28	189	13	1764	21	AAA08564				
C	29	183	12	378	22	AAF65696				
C	30	182	12	1413	23	ABL05597				
C	31	179	12	1645	22	AAS27141				
C	32	173	12	323	22	AAL14193				
C	33	172	12	323	22	AAL31055				
C	34	173	12	4103	23	ABL05586				
C	35	172.5	12	1993	25	ABX55986				
C	36	172.5	12	239	23	ABV4898				
C	37	177.5	12	3001	24	ABZ25537				
C	38	172	12	1046	22	AAS27514				
C	39	171	11	2918	25	ABT13422				
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XX	Nucleotide sequence of a human chaperone polypeptide.		Nucleotide sequence of a human chaperone polypeptide.		Nucleotide sequence of a human chaperone polypeptide.					
XX	RESULT 1		RESULT 1		RESULT 1					
XX	DT		DT		DT					
XX	Nucleotide sequence of a human chaperone polypeptide.		Nucleotide sequence of a human chaperone polypeptide.		Nucleotide sequence of a human chaperone polypeptide.					
XX	Human; chaperone polypeptide; reproductive disease; prolactin production;		Human; chaperone polypeptide; reproductive disease; eye disorder; Glaucoma;		Human; chaperone polypeptide; reproductive disease; eye disorder; Glaucoma;					
XX	infection; tumour; cancer; Peyronie's disease; keratitis; neuromuscular disorder; cystic fibrosis;		infection; tumour; cancer; Peyronie's disease; eye disorder; Glaucoma;		infection; tumour; cancer; Peyronie's disease; eye disorder; Glaucoma;					
XX	conjunctivitis; keratitis; inflammatory disorder; Zellweger syndrome; Addison's disease; iritis;		conjunctivitis; keratitis; inflammatory disorder; Zellweger syndrome; Addison's disease; iritis;		conjunctivitis; keratitis; inflammatory disorder; Zellweger syndrome; Addison's disease; iritis;					
XX	metabolic disorder; autoimmune disorder; systemic lupus erythematosus;		metabolic disorder; autoimmune disorder; systemic lupus erythematosus;		metabolic disorder; autoimmune disorder; systemic lupus erythematosus;					
XX	acquired immunodeficiency syndrome; AIDS; asthma; atherosclerosis;		acquired immunodeficiency syndrome; AIDS; asthma; atherosclerosis;		acquired immunodeficiency syndrome; AIDS; asthma; atherosclerosis;					
XX	cell proliferative disorder; gene therapy; ss.		cell proliferative disorder; gene therapy; ss.		cell proliferative disorder; gene therapy; ss.					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



XX	12-SEP-2000; 2000US-232104P.	Qy	101 ThrMetMetCysSerArgCysGlnGlyLysSerArgArgPheGluLeuAspArgGluPro 120
PR		Db	765 ACTAGATGCTGATGGGTGAACTGGCATCCAAAGGATTCAGGAGCTTGAATGGACCGGAACTT 824
XX	(HUMA-) HUMAN GENOME SCI INC.	Qy	121 LysSerAlaArgTrpCysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspPhe 140
PA	Komatbolis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;	Db	825 AAGACTGCCGATACTGCTGAGTTTAATGGCTCAACCTGCTAGGAGAACCTGAGGAGAC 884
XX	Rosen CA, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;	Qy	141 TrpAlaGluUserSerMetLeuGlyLeuLysIsoleThrTYrPheAlaLeuMetAspGlyLys 160
PI	Ni J;	Db	885 TGGCAGAGTCAAAGCTGATGGCCCTCAAGATCACCTACTTGCACTGTATGGATGAAAG 944
PI	DR WPI: 2002-258041/30.	Qy	161 ValTyrAspIleLeuIleGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHis 180
DR	?-PSDB; ABB77019.	Db	945 GTGTATGACATCACAGTCAGGGCTGAGCTGTAGGTATCTCCCAGATACCCAC 1004
XX	New nucleic acid molecules encoding 22 human secreted proteins for diagnosing or treating e.g. autoimmune diseases, hyperproliferative disorders, and cardiovascular disorders, and used as food additives or preservatives -	Qy	181 ArgValProTyroHisIleSerPheGlySerArgIleProGlyThiArgGlyArgGlnIarg 200
PS	Disclosure: Page 451-452; 526PP; English.	Db	1005 AGAGTCCCATTACATCTATTGTTCTGGATTCAGGACCCAGAGGCGGAGAGA 1064
XX	The sequence represents a cDNA sequence of the invention, isolated from human clone ID HNTBP82. The invention relates to novel isolated nucleic acid molecules encoding 22 human secreted proteins. The proteins of the invention have immunosuppressive, antiinflammatory, antineoplastic, antiproliferative, cytostatic, carcinant, vasotropic, cerebroprotective, antibiotic, virucide, fungicide, ophthalmological, and vulnerary activity. The polynucleotides may have a use in gene therapy. The polynucleotides and polypeptides encoded by them are used to prevent, treat or ameliorate a medical condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation. The polypeptides can also be used as a food additive or preservative.	Qy	201 AlaThrProAspAlaProProAlaAspLeuSerArgIlePheGlnVal 220
CC	RESULT 3	Db	1065 GCCACCCAGATGCCCTCTGCCTATCAGATTCTGAGTGGATCTTCAGATA 1124
CC	ABL56700	Qy	221 ProProGlyLysMetIleAngIlysAsnProAlaProGlnDroAlaProGlyAla 240
CC	ID ABL56700 standard; cDNA; 3286 BP.	Db	1125 CCCCGGGCGATGGCCAAATGGAACTCTGGCTCTCAGCTGCCCTGAGCC 1184
CC	XX	Qy	241 AlaAlaAlaSerLysProAsnSerThrValProGlyGluAlaLysProLysArg 260
CC	AC ABL56700;	Db	1185 GCTGCAGCCCTTAAGCCAAAGCAJAGTACCAAGGGAGAGCAACCTAAGCT 1244
CC	XX	Qy	261 LysLysValArgArgProPheGlnIarg 269
CC	XX	Db	1245 AAGAAAGTGGAGGGCCCTCCAAACGT 1271
CC	DT 30-JUL-2002 (first entry)	XX	
CC	XX	XX	Nucleotide sequence of human P125-77.22 polypeptide.
CC	DE	XX	Human; P125-77.22; mucosal disease; BVDV infection; gene therapy;
CC	KW	XX	gene; ss.
CC	KW	XX	Homo sapiens.
CC	OS	XX	
CC	XX	XX	Location/Qualifiers
CC	Key	XX	122..2230
CC	FT	XX	/*tag= a
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CC	PN	XX	WO200226810-A1.
CC	PD	XX	04-APR-2002.
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CC	XX	XX	10-SEP-2001; 2001WO-CN01354.
CC	XX	XX	12-SEP-2000; 2000CN-0125190.
CC	PR	XX	(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
CC	PA	XX	Mao Y, Xie Y;
CC	XX	XX	DR WPI; 2002-281319/32.
CC	DR	XX	P-PSDB; ABB7732.
CC	XX	XX	Protein P125-77.22 and encoding polynucleotide, used in diagnosis and treatment of human mucosal disease caused by BVDV infection -
CC	PT	PT	

XX	Claim 6; Page 27-29; 33pp; Chinese.	Db	2201 AAGAAAGTAGGAGCCCTCAACGT 2227
PS	The present sequence encodes human PI25-77-22 polypeptide. The peptide and polynucleotide are used in diagnosis and treatment of human mucosal disease caused by viral BvPy (undefined) infection. The polynucleotide may also be used for gene therapy.	RESULT 4 AAI96802 standard; cDNA; 747 BP. ID AAI96802 XX	
XX	Sequence 3286 BP; 787 A; 785 C; 895 G; 819 T; 0 other;	AC	AAI96802;
SQ	Alignment scores: Pred. No.: 2.3e-115 Length: 3286 Score: 1430.00 Matches: 268 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 99.63% Mismatches: 0 Query Match: 99.79% Indels: 0 DB: 24 Gaps: 0	XX	Human neuroblastoma expressed polynucleotide SEQ ID NO 2877. DE Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
US-10-049-742-11 (1-269) × ABL56700 (1-3286)	XX	XX	XX Human neuroblastoma expressed polynucleotide SEQ ID NO 2877. DE Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
Qy 1 MetAlaGlyValProGluAspGluLeuAsnProPheHisValLeuGlyValGluAlaThr 20	PD	13-SSP-2001.	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
Db 1421 ATGGCTCGTTCCTGAGATCAGTAAACCTTTCATGTACTGGGGTGAGGCCACA 1480	PF	02-MAR-2001; 2001WO-JP01629.	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
. Qy 21 AlaSerAspValGluLeuLysIysAlaTyrrArgGlnLeuAlaValMetValHisProAsp 40	PR	07-MAR-2000; 2000JP-0159195.	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. PA (CHIBA) CHIBA PREFECTURE (HISIM) HISAMITSU PHARM CO LTD.
Db 1481 GCATCAGATGTTGAACCTGAGGAGGCCTATAACAGCTGGCATGTGGTCATCTGAC 1540	PA		XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. PA (CHIBA) CHIBA PREFECTURE (HISIM) HISAMITSU PHARM CO LTD.
Qy 41 LysAsnIleHisProArgAlaGluGluLysAlaPhaLysValLeuArgAlaAlaPapile 60	PI		XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. PA (CHIBA) CHIBA PREFECTURE (HISIM) HISAMITSU PHARM CO LTD.
Db 1541 AAATATCATCCCCGGCTCAGGGCTCTAACGGTTCAGGCTCAAGTTTGCGAGCACATTGGACAT 1600	DR	WPI: 2001-565584/63.	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
Qy 61 ValSerAsnAlaGluLysArgLysGluTrgIumEtLysArgMetAlaGluAsnGluLeu 80	PT		XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. PT useful as probe or primer in diagnosing Prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker for anti-cancer agents -
Db 1601 GTCAAGCATGCTGAAAGCAGAAGGATGAGATGAGAACGATGAGATGAGATGAGCTG 1660	PT		XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. PT useful as probe or primer in diagnosing Prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker for anti-cancer agents -
Qy 81 SerArgSerValAsnGluPhaLeuSerLysIleGluLysPheAspLeuLysGluAlaMetAsn 100	XX	Claim 1; Page 2103; 2979pp; Japanese.	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
Db 1661 AGCGGGTCATGTTCTGTCCTAAAGATGACTCAAGTCAGCTCAAGGGCAATGAA 1720	CC		CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
Qy 101 ThrMetMetCysSerArgCysGlnGlyLysIhsIhsArgArgPheGluLysAspGluPro 120	CC		CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
Db 1721 ACTATGAATGTTGAGCCGAGCAGGAAAGCATAGGGTTGAAAGGACGGGAACT 1780	CC		CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
Qy 121 LysSerAlaArgTyrCysAlaGluCysAsnArgLeuHisProAlaGluGlyAspPhe 140	CC		CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
Db 1781 AAGAGTGCTGAGAFACTGCTGACTGCTGACTGTAAATGGCTCATCTGTGAGAAAGGAGACTT 1840	CC		CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
Qy 141 TrpAlaGluUserSerMethLeuGlyLeuLysIleThrPheAlaLeuMetLysGlyLys 160	XX	Alignment Scores:	XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss. XX Homo sapiens.
Db 1841 TGGCAGAGTCAAAGCATGTTGGCCCTCAAGATCACCTTTGCACITGATGGAAAG 1900	Pred. No. :	2.51e-88	Length: 747
Qy 161 ValTyrAspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThr 180	Score:	1112.00	Matches: 216
Db 1901 GTGTATGACATACAGGGGGATGGATCAGGTGGCTCAGGATACCCAC 1960	Percent Similarity:	91.21%	Conservative: 2
Qy 181 ArgValPheCtyRhsIleSerPheGlySerArgIleProGlyThrArgGlyArgGlnArg 200	Best Local Similarity:	90.38%	Mismatches: 19
Db 1961 AGAGTCCCCTATCACATCATTGGTCAGGCCACAGGGCGAGAG 2020	Query Match:	77.60%	Indels: 3
Qy 201 AlaThrProAspAlaProProAlaAspLeuSerArgIlePheGlnVal 220	DB:	22	Gaps: 1
Db 2021 GCAACCCGAGATGCCCTCTGCTGATCTTCAGGATTCTGATTCAGTA 2080			
Qy 221 ProProGlyGlnMetProAsnGlyAsnPhePheAlaAlaProGlnProGlyAla 240			
Db 2081 CCCCCAGGGCAGATGCCCTATGGAACTTCTGAGCCTCAGGCCCTGGAGCC 2140			
Qy 241 AlaAlaAlaSerLysProLysSerThrValProLySGLyLysProLysArgArg 260			
Db 2141 GCTCAGGCCTCTAACGCCAACGACAGTACGCCAGGGAAAGGCCAACCTAACGGGG 2200			
Qy 261 LysLysValArgArgProBheGinArg 269			
Db 216 ATGGCAGAAATGAGCTAGGCGGTAGTAATGAGTTCTGTCAGAACGTCAGATGAC 275			

Qy	95	LeuLysGluAlaMetAsnThrMetCysSerArgCysGlnGlyLysSerArgArgPhe	114
Db	276	CTCAAGGGCATGATGAACTATGATGTGGTAGCGCAGGAAGCATGGAGTTT	335
Qy	115	GlumetaAspArgCysProLysSerAlaArgTyrcysAlaGlucysAsnArgLeuHisPro	134
Db	336	GAAATGACCGAACCTAAGTGCCAGATACTGTCAGTGTAAATTGGTGCATCT	395
Qy	135	AlaAlaGluLysGlyAspPheTrpAlaGluSerSerMetLeuGlyLeuLysSerIleThrTyrPhe	154
Db	396	GCTGAGGGAGGGACATTTGGAGAGTCAGATGTGGCTCAAGATCACCTACTT	455
Qy	155	AlaLeuNetAspGlyLysValTyraSpaIleSerPheGlySerArgIleProGln	174
Db	456	GCACTGATGGATGAAAGGTGATGACATCACAGTGGCTGGATSOCAGCGTAGG	515
Qy	174	VilleSerProAspThrHisArgValProTyrrHisIleSerPheGlySerArgIleProGln	194
Db	516	TATCTCCCAAGATACCACAGTCCCCTATCACATCTATTGGTCTCGATTCCAGG	575
Qy	194	YThrArgGlyArgGlnArgAlaIleThrProAspAlaProProAlaAspPheLe	214
Db	576	CACCAAGGCCAGCAGAGCCACCCCCAGATGCCCTCTGCTGATCTTCAGATTCTT	635
Qy	214	UserArgIlePheGlnValProProGlyGlnMetProAsnIlePheAlaAlaP	234
Db	636	GAGTCGAATCTTCAGTACCCAGGGCANATGCCCATGGAAACTCTTGCAGTT	695
Qy	234	oGlnProAlaProGlyAlaAlaAlaAlaSerIleProAsnSerThrValProLys	252
Db	696	TAA-CCFTGCCCTGGACCCTGGTAANCTNTAACG--CAACAGNACATACCAAAG	746
<b>RESULT 5</b>			
ID	A0Z34492	standard; cDNA; 754 BP.	
XX	A0Z34492;		
AC			
XX			
DT	01-FEB-2000	(first entry)	
XX			
DE	Human LYST interacting protein LIP6 cDNA.		
XX			
KW	LYST; human; LYST-2; LYST interacting protein; lysosome; CHS; Chediak-Higashi syndrome; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; inflammatory bowel disease; diabetes mellitus; multiple sclerosis; atopic disease; asthma; hay fever; rhinitis; urticaria; nasal polyp; cancer; viral disease; neurodegenerative disease; pigmentary disorder; viral disease; platelet dysfunction; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CDS	11..56 /*tag= ^ /partial		
XX	W09951741-A2.		
PN			
XX			
PD	14-OCT-1999.		
XX			
PT	29-MAR-1999;		
XX	99WO-US06831.		
PR	03-APR-1998;		
XX	98US-0054956.		
PA	(CURAGEN CORP.		
XX			
PI	Nandabalan K, Kingsmore S;		
XX			
DR	WPI; 1999-620203/53.		
XX	P-PSDB; AAY32126.		
QY	229 AsnPhePheAlaAlaProGlnProAlaProGlyAlaAlaAsnSerLysProAsnSer		
XX	248		

PT Protein complexes, interacting proteins, and related polynucleotides  
 PT for treating and preventing e.g. atopic, autoimmune or neurodegenerative diseases -  
 XX

Claim 21; Fig 7: 172BP; English.

XX This is the nucleotide sequence of cDNA which codes for a novel human LYST interacting protein, LIP6 (see AAY32126), that shows homology to Pescivirus NS2-3. LYST is the human lysosomal Chediak-Higashi syndrome (CHS) protein. The invention relates to complexes of LYST or LYST-2 (see A0Z34492) with proteins identified as interacting with LYST or LYST-2 by a modified yeast two-hybrid assay system. The interacting proteins include 10 novel proteins, LIP1-10 (see AAY32121-30). Methods of screening the protein complexes for efficacy in treating and/or preventing atopic diseases (e.g. asthma, nasal polyps, hay fever, rhinitis, urticaria), autoimmune diseases (e.g. CHS, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, diabetes mellitus, multiple sclerosis), neurodegenerative disease, certain forms of cancer, pigmentation disorders, Platelet dysfunction and viral diseases are provided. Nucleic acids (see AAY34487-96) encoding LIP1-10, modulation of LIP function by gene therapy, use of antisense oligonucleotides for suppression of LIP protein expression, screening for agonists and antagonists, diagnosing or screening for the presence of a predisposition to a disease or disorder, and animal models are also disclosed.

XX Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;

XX SQ Alignment Scores:  
 Pred. No.: 5.55E-83  
 Score: 5.55E-83  
 Length: 754  
 Matches: 1051.00  
 Percent Similarity: 99.50%  
 Best Local Similarity: 99.50%  
 Conservatve: 0  
 Mismatches: 1  
 Query Match: 73..34%  
 DB: 20  
 Gaps: 0

XX US-10-049-742-11 (1-754) x AAY34492 (1-754)

Qy 69 GlutYGlumethylsArgMetAlaGluAsnGluLeuSerArgSerValAsnGluPheLeu 88  
 Db 2 GAACTGATGAAAGATGAAAGATGCTGAGATGAGATGAGCTGAGCCGTGAGTAATGAGTCTG 61

Qy 89 SerLysLeuGlnAspAspLeuLysGluAlaMetAsnThrMetCysSerArgCysGln 108  
 Db 62 TCCAAAGCTGCAACATGACCTCAAGGCCAAATGAAATACTATGATGTAGCCCATGCCAA 121

Qy 109 GlyLysHisArgGargPhGluIleProLysSerAlaArgTyrcysAlaGlu 128  
 Db 122 GGAAAGCATAGGAGCTTGAATGGACCCGAACTTAAGAGGCCAGTACTGTGCTGAG 181

Qy 129 CysAsnArgLeuHisProAlaGluGluGlyAspPhePheAlaGluUserSerMetLeuGly 148  
 Db 182 TGTAATGGCTGATCCGCTGAGGAGGAGCTTGGCAGAGTCAGAATGAGTGTGAGC 241

Qy 149 LeuLysIleThrYrPheAlaLeuMetAspGlyLysValTyrAspIleThrGluTrpAla 168  
 Db 302 GGTGCCRGGCTGTTGATCTCCCGATACCCAGATCCACATCTCCTT 361

Qy 189 GlySerArgIleProGlyThrArgGlyArgGlnArgAlaIleThrProAspAlaProProAla 208  
 Db 362 GGTCTCGGATTCAAGGACCCAGAGGCCCCAGATGCCCCCTCTCTCT 421

Qy 209 AspLeuGlnAspPheLeuSerArgIlePheGlnValProProGlyGlnMetProAsnGly 228  
 Db 422 GATCTCAGGATTCTTGAGTGGATCTTCAAGTACCCAGGGAGATGCCAAAT-GGG 480

Qy 229 AsnPhePheAlaAlaProGlnProAlaProGlyAlaAlaAsnSerLysProAsnSer 248

Db	481	AACITCTTGAGCTTCTAGCCCTGCCCTGGAGCGCTCAGGCCAACAGC 54
Qy	249	Thr Val Pro Lys Gly Glu Ala Lys Pro Lys Arg Arg Lys Val Arg Arg Pro The Gln 268
Db	541	ACACTACCAAAGGAAAGCCAAACCTAAGGGCGAAGAAATGAGGAGGCCCTCCAA 600
Qy	269	Arg 269
Db	601	CGT 603
RESULT 6		
ABX04184	ID	ABX04184 standard; cDNA; 754 BP.
XX	XX	Human mRNA differentially expressed in mesenchymal cells #31.
DE	XX	Human ss: gene; skeletal growth; cartilage degeneration disorder;
KW	XX	chondroblastic phenotype; mesenchymal cell; cartilage formation;
KW	XX	cartilage formation; arthritis; osteoarthritis; rheumatoid arthritis;
KW	XX	gout; arthritis; adjuvant arthritis; arthrosis; deformans; antigen;
KW	XX	infectious arthritis; osteochondrosis; RDA; antiarthritic; osteopathic;
KW	XX	antirheumatic; antiinflammatory; representational difference analysis.
OS	XX	Homo sapiens.
XX	PN	WO200271927-A2.
XX	PD	19-SEP-2002.
XX	PF	12-MAR-2002; 2002WO-US07787.
XX	PR	12-MAR-2001; 2001US-274980P.
XX	PA	(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
XX	PI	Yates KE, Mizuno S, Glowacki J;
XX	DR	WPI; 2002-722276/78.
XX	PT	New nucleic acid molecules capable of promoting chondrogenesis, useful
PT	PT	for diagnosing and treating cartilaginous tissue degeneration
PT	PT	conditions, e.g. osteoarthritis, rheumatoid arthritis, gout arthritis,
PT	PT	or osteochondrosis -
XX	PS	Claim 33: Page 129; 153pp; English.
XX	CC	The invention relates to new isolated nucleic acid molecule comprising a
CC	CC	nucleic acid molecule consisting of a gene differentially expressed
CC	CC	in cells undergoing differentiation from mesenchymal cell to a
CC	CC	chondroblastic phenotype, or hybridising under stringent conditions
CC	CC	to them (or their fragments). Also included are expression vectors,
CC	CC	transformed host cells, expressed polypeptides or peptide fragments
CC	CC	(which induce differentiation of a mesenchymal cell and may be used as an
CC	CC	immunogen), binding partners of the polypeptides, a method for
CC	CC	identifying an agent useful in modulating mesenchymal cell
CC	CC	differentiation induction activity of a molecule, a method of diagnosing
CC	CC	a condition characterized by aberrant expression of a nucleic acid
CC	CC	molecule or its expression product; a method for determining regression,
CC	CC	progression or onset of cartilaginous tissue degeneration condition in a
CC	CC	subject characterised by aberrant expression of a nucleic acid molecule
CC	CC	or its expression product, a method for treating a cartilaginous tissue
CC	CC	degeneration condition, a method for treating a subject to reduce the
CC	CC	risk of cartilaginous tissue degeneration condition developing in the
CC	CC	subject, a method for identifying a candidate agent for treating a
CC	CC	cartilaginous tissue degeneration condition, and a solid-phase nucleic
CC	CC	acid molecule array consisting essentially of a set of nucleic acid
CC	CC	molecule as cited above (or known from known genes shown to be
CC	CC	differentiably expressed in developing mesenchymal cells using the
CC	CC	technique of representational difference analysis, RDA), its expression

CC products or fragments, fixed to a solid substrate. The nucleic acids, CC polypeptides and agents are useful for treating cartilaginous tissue CC degeneration conditions such as osteoarthritis, rheumatoid arthritis, CC gout arthritis, adjuvant arthritis, arthritis deformans, infectious CC arthritis or osteochondrosis. The present sequence is a cDNA from CC a known gene differentially expressed in developing mesenchymal cells.

**RESULT 6**

ABX04184	Human mRNA differentially expressed in mesenchymal cells #31.
ID: ABA04184 standard; cDNA; 754 BP.	
XX	
XX	10-JAN-2003 (first entry)
XX	
DE	
KW	Human; 5S; Gene; Skeletal growth; cartilage degeneration disorder;
KW	chondroblastic phenotype; mesenchymal cell; cartilage formation;
KW	bone formation; arthritis; osteoarthritis; rheumatoid arthritis;
KW	gout; arthritis; adjuvant; arthritis; arthritis deformans; antigen;
KW	infectious arthritis; osteochondrosis; RDA; antiarthritic; osteopathic;
KW	antirheumatic; antiinflammatory; representational difference analysis.
XX	
OS	Homo sapiens.
XX	
PN	WO200271927-A2.
XX	
PD	19-SEP-2002.
XX	
PP	12-MAR-2002; 2002WO-US027787.
XX	
PR	12-MAR-2001; 2001US-274980P.
XX	
PA	(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
PA	
P1	Yates KB, Mizuno S, Glowacki J;
XX	
DR	WPI; 2002-7232276/78.
XX	
PT	New nucleic acid molecules capable of promoting chondrogenesis, useful
PT	for diagnosing and treating cartilaginous tissue degeneration
PT	or osteoarthritis, rheumatoid arthritis, gout arthritis,
PT	or osteochondrosis -
XX	
PS	Claim 33; Page 129; 153pp; English.
XX	
CC	The invention relates to new isolated nucleic acid molecule comprising a
CC	nucleic acid molecule consisting of a gene differentially expressed
CC	in cells undergoing differentiation from mesenchymal cell to a
CC	chondroblastic phenotype, or hybridising under stringent conditions
CC	to them (or their fragments). Also included are expression vectors,
CC	transformed host cells, expressed polypeptides or peptide fragments
CC	(which induce differentiation of a mesenchymal cell and may be used as an
CC	immunogen), binding partners of the polypeptides, a method for
CC	identifying an agent useful in modulating mesenchymal cell
CC	differentiation induction activity of a molecule, a method of diagnosing
CC	a condition characterized by aberrant expression of a nucleic acid
CC	molecule or its expression product; a method for determining regression,
CC	progression or onset of cartilaginous tissue degeneration condition in a
CC	subject characterised by aberrant expression of a nucleic acid molecule
CC	or its expression product, a method for treating a cartilaginous tissue
CC	degeneration condition, a method for treating a subject to reduce the
CC	risk of cartilaginous tissue degeneration condition developing in the
CC	subject, a method for identifying a candidate agent for treating a
CC	cartilaginous tissue degeneration condition, and a solid-phase nucleic
CC	acid molecule array consisting essentially of a set of nucleic acid
CC	molecule as cited above (or known from known genes) cells using the
CC	differentially expressed in developing mesenchymal cells using the
CC	technique of representational difference analysis, RDA).

KW	Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis;
KW	Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder;
KW	non-tuberculous granulomatous orchitis; connective tissue disorder; birth disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss;
XX	
OS	Homo sapiens.
XX	
PN	WO200271928-A2.
XX	
PD	19-SEP-2002.
XX	
PF	14-MAR-2002; 2002KO-US07826.
XX	
PR	14-MAR-2001; 2001US-276025P.
PR	14-MAR-2001; 2001US-276026P.
PR	10-AUG-2001; 2001US-31132P.
PR	19-SEP-2001; 2001US-32380P.
PR	26-SEP-2001; 2001US-324967P.
PR	26-SEP-2001; 2001US-325102P.
PR	26-SEP-2001; 2001US-325149P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.

ahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB, Ter RC, Lu K, Schmandt RE, Zhao X, Giatt K; ; 2002-723277/78.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing an expression level of a cancer marker in a sample from a patient and in a non cancer patient -

present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing expression level of a marker in a patient sample and the normal level expression of the marker in a control non-ovarian cancer sample, where marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), particular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis or attherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the invention.

xx	Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;
SQ	
Alignment Scores:	
Prod. No. :	5.55e-83
Score:	1051.00
Percent Similarity:	99.50%
Percent Conserved:	99.50%
Length:	754
Matches:	200
Conservatives:	0

Best Local Similarity:	99.50%	Mismatches:	1
Query Match:	73.34%	Indels:	1
DB:	24	Gaps:	0
US-10-049-742-11 (1-269) × ABS76460 (1-754)			
Qy	69 GlutylgluMetLysArgMetAlaGluIuAsnGluLeuSerArgSerValAsnGluPheLeu	DB:	88
Db	2 GAGTAGATAGATAAAACAACTGGAGAAGTGTAGCTTAATGAGTTTC	Db:	61
Qy	89 SerLysIleGlnAspAspLeuLysGluAlaMetAsnThrNetMetCysSerArgCysGln	Qy:	108
Db	62 TCCAAGTGCGATGACTCTAAGGGCATGAACTAAGTGTAGCGATGCCAA	Db:	121
Qy	109 GlyLysIleGlnProAlaGluIuGlyAspPheTrpAlaGluUserSerMetLeuGly	Qy:	128
Db	122 CGAAAGCATGGAGGTGTTGAAATGGACCAGGAAACCTAACAGTGCAGATACTGTGTGAG	Db:	181
Qy	129 CysAsnAsnArgLeuHisProAlaGluIuGlyAspPheTrpAlaGluUserSerMetLeuGly	Qy:	148
Db	182 TGTATATGGCTGATCTGTGAGACTTGGAGAGACTTGGAGAGTCAGATGTGGC	Db:	241
Qy	149 LeuLysIleThrPheAlaLeuMetAspGlyLysValtyrAspIleThrGluTrpAla	Qy:	168
Db	242 CTCAGATCACCTACTTTGCACTGATTGATGGATCGAAAGCTGTATGACATCACAGAGGGCT	Db:	301
Qy	169 GlyCysGlnArgValGlyIleSerProAspThrHisArgValProTyRHisIleSerPhe	Qy:	188
Db	302 GGATGCCAGGTGTAGTATCTCCAGATPACCCACAGAGTCCCCATCACATCTCATTT	Db:	361
Qy	189 GlySerArgIleProGlyThrArgGlyArgGlnArgAlaThrProAspAlaProProAla	Qy:	208
Db	362 GTCCTCTGGATTCAGGCCACAGAGCCGGAGAARGGCCACCCCGATGCCCTCTGTCT	Db:	421
Qy	209 AspLeuGlnAppPhalLeuSerArgIlePheGlnValProProGlyGlnMetProAsnGly	Qy:	228
Db	422 GATCTTCAGGATTCTTGAGTCGGATCTTCAGGTCAGTCCAACTGGCAAT-TGGG	Db:	480
Qy	229 AsnPheIleAlaAlaProGlnProAlaProGlyIaAlaAlaAlaIaserLysProAsnSer	Qy:	248
Db	481 AACCTCTTGTGAGCTCTCAGCTGCCCCTGAGCCCTGGAGCTCTAGCCCAACAGC	Db:	540
Qy	249 ThrValProLysGlyGluAlaLysProLysArgArgLysLysValArgArgProProGln	Qy:	268
Db	541 ACAGTACCCAACTGGAGAACCTAACGGCCAAAGAAAGTGGAGGCCCTCCCAA	Db:	600
Qy	269 Arg 269	Qy:	
Db	601 CGT 603	Db:	
RESULT 8			
AAS30481	standard; DNA; 7453 BP.	ID	
XX		XX	
AC		XX	
DT	21-NOV-2001 (first entry)	XX	
DE	DNA encoding novel prostate gland antigen, Seq ID No 339.		
XX			
KW	Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;		
KW	antianæmic; dermatological; immunosuppressive; antiinflammatory;		
KW	antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic;		
KW	osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;		
KW	prostatic; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;		
KW	hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;		
KW	reproductive system disorder; autoimmune disorder; urinary system;		
KW	systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;		
KW	blood-related disorder; hyperproliferative disorder; respiratory;		
KW	neurological disorder; endocrine disorder; inflammatory disorder;		
KW	liver disorder; wound healing; food preservative; ds.		
XX			

XX WO200155447-A1.  
 PN 2000US-0235836.  
 XX PR 29-SEP-2000; 2000US-0233627.  
 PD PR 29-SEP-2000; 2000US-0233667.  
 XX PR 29-SEP-2000; 2000US-0233659.  
 PF PR 29-SEP-2000; 2000US-0233670.  
 XX PR 02-OCT-2000; 2000US-0233687.  
 PR PR 02-OCT-2000; 2000US-0237037.  
 04-FEB-2000; 2000US-0180628.  
 PR PR 02-OCT-2000; 2000US-0237038.  
 02-MAR-2000; 2000US-0184664.  
 PR PR 02-OCT-2000; 2000US-0237039.  
 16-MAR-2000; 2000US-0186350.  
 PR PR 02-OCT-2000; 2000US-0237040.  
 17-MAR-2000; 2000US-0189874.  
 PR PR 13-OCT-2000; 2000US-0239935.  
 PR 18-APR-2000; 2000US-0190076.  
 PR PR 13-OCT-2000; 2000US-0239937.  
 19-MAY-2000; 2000US-0198123.  
 PR PR 20-OCT-2000; 2000US-0240960.  
 07-JUN-2000; 2000US-0205515.  
 PR PR 20-OCT-2000; 2000US-0237040.  
 28-JUN-2000; 2000US-0209467.  
 PR PR 20-OCT-2000; 2000US-0241786.  
 30-JUN-2000; 2000US-0214886.  
 PR PR 20-OCT-2000; 2000US-0241787.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR PR 20-OCT-2000; 2000US-0241808.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR PR 20-OCT-2000; 2000US-0241809.  
 11-JUL-2000; 2000US-0217487.  
 PR PR 20-OCT-2000; 2000US-0241826.  
 11-JUL-2000; 2000US-0217496.  
 PR PR 01-NOV-2000; 2000US-0241785.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR PR 08-NOV-2000; 2000US-0241786.  
 26-JUL-2000; 2000US-0215135.  
 PR PR 08-NOV-2000; 2000US-0241787.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR PR 08-NOV-2000; 2000US-0244776.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR PR 08-NOV-2000; 2000US-0244777.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR PR 08-NOV-2000; 2000US-0244778.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR PR 08-NOV-2000; 2000US-0244523.  
 PR 14-AUG-2000; 2000US-0218290.  
 PR PR 08-NOV-2000; 2000US-0244524.  
 PR 14-AUG-2000; 2000US-0220963.  
 PR PR 08-NOV-2000; 2000US-0244525.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR PR 08-NOV-2000; 2000US-0244526.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR PR 08-NOV-2000; 2000US-0244527.  
 PR 22-AUG-2000; 2000US-0225270.  
 PR PR 08-NOV-2000; 2000US-0244528.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 14-AUG-2000; 2000US-02255214.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 14-AUG-2000; 2000US-02255266.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 14-AUG-2000; 2000US-0225567.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 14-AUG-2000; 2000US-0225568.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 23-AUG-2000; 2000US-0227182.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 10-AUG-2000; 2000US-0228924.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 01-SEP-2000; 2000US-0229387.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR PR 08-NOV-2000; 2000US-0244532.  
 PR 03-SEP-2000; 2000US-0229509.  
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 PR 14-SEP-2000; 2000US-0231243.  
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 PR PR 25-SEP-2000; 2000US-0234997.  
 PR 26-SEP-2000; 2000US-0235484.  
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XX

PA



Db 3494 GCGGAAGAAACTGAGGGCCCTTCCAAAGT 3524

RESULT 9  
 AAL06261  
 ID AAL06261 standard; DNA; 7453 BP.  
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 AC AAL06261;  
 XX DT 21-NOV-2001 (first entry)  
 XX DE Human reproductive system related antigen DNA SBQ ID NO: 8949.  
 XX Human; reproductive system related antigen; reproductive system disorder;  
 KW cancer; gene therapy; ds.  
 XX OS Homo sapiens.  
 XX PN WO2000153320-A2.  
 XX PD 02-AUG-2001.  
 XX PF 17-JAN-2001; 2001WO-US01339.  
 XX PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
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 PR 17-MAR-2000; 2000US-0190076.  
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 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
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 PR 11-JUL-2000; 2000US-0217487.  
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 PR 14-AUG-2000; 2000US-0225268.  
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 PR 14-SEP-2000; 2000US-0232397.  
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 PR 08-NOV-2000; 2000US-0244894.  
 PR 08-NOV-2000; 2000US-0244895.  
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PR	01-DEC-2000;	2000US-0250160.	Db	2415	CGATGCCAAGGAAAGCATAGGTATAATGAGGAGGGATGGCAATTACAGCTCA	2474
PR	01-DEC-2000;	2000US-0250391.	Qy	111	- - - - -	111
PR	05-DEC-2000;	2000US-0251030.	Db	2475	GGGATATGTAACCAAGGATCCTCTAGTGAGTACTGCTTAATTAGTGAATTACATCTGTAT	2534
PR	05-DEC-2000;	2000US-0251988.	Qy	111	- - - - -	111
PR	05-DEC-2000;	2000US-0256719.	Db	2535	CTCATATTAGTAAAAGACCCTTAAGTTCTACCTTGTCAATTGTCATAGACTGAC	2594
PR	06-DEC-2000;	2000US-0251479.	Qy	111	- - - - -	111
PR	08-DEC-2000;	2000US-0251856.	Db	2595	GATTTAATTAGCACTAAGAAACATAGCTTTAGGATAGAACCTTGAACGGATATGAAAT	2654
PR	08-DEC-2000;	2000US-0251868.	Qy	111	- - - - -	111
PR	08-DEC-2000;	2000US-0251869.	Db	2655	ACTAAGTGGGTAATTAGATGTTAGCCCTATTCTGTAATATGCTAAGCTACTAG	2714
PR	08-DEC-2000;	2000US-0251989.	Qy	111	- - - - -	111
PR	11-DEC-2000;	2000US-0251990.	Db	2655	ACTAAGTGGGTAATTAGATGTTAGCCCTATTCTGTAATATGCTAAGCTACTAG	2714
PR	11-DEC-2000;	2000US-0254097.	Qy	112	- - - - -	ArgR 113
PR	05-JAN-2001;	2000US-0229678.	Db	2715	CAGTGCCTAGGTAGGCTTGACAAATTATTAGGAACATATCCCTTGTTGGTGCAGGAG	2774
XX	(HUMA - ) HUMAN GENOME SCI INC.	XX	Qy	113	qPheGluMetAsPArgGluProLysSerAlaArgTrpAlaGluCysAsnArgLeuHi	133
PS	SEQ ID NO: 8949;	1297 bp + Sequence Listing; English.	Db	2775	GTGGAATGGACGGAACCTAAGTGGCGATCTGTGAGGTAAATGGCTGCA	2814
XX	The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.	XX	Qy	133	sProAlaGluGluGlyAspPheTrpAlaGluUserSerMetLeuGlyIeuLysIleThrty	153
CC	CC	CC	Qy	133	GlutPheLeuSerAsnAlaGluCysGlnArgValGlyIleSerProAspThrHisAR	181
CC	CC	CC	Db	2835	TCCCTGCTGAGGAGAACATTGGCAGAGCTGTCGGCCCAAAGAACCCCTA	2894
XX	Sequence 7453 BP; 1980 A; 1633 C; 1692 G; 2147 T; 1 other;	XX	Qy	153	rPheAlaLeuIleAspGlyLysValTyAspIleThr-----	165
SQ	US-10-049-742-11 (1-263) x AAL06261 (1-7453)	Db	2895	CTTGTGACTGTAGGATGAAAGGTATGACATCACAGSTACTCTGTCTCTAGAAAT	2954	
Pred.	No.:	2,236-78	Length:	165	- - - - -	
Score:	1012.50	Matches:	7453			
Percent Similarity:	45.21%	Conservative:	231			
Best Local Similarity:	45.21%	Mismatches:	0			
Query Match:	70.66%	Indels:	2			
DB:	22	Gaps:	4			
Db	2015	TCTCATCTTTAGGGCTGGATGAGGTAGATCTCCCGATACCCAGATCCACAG	3074			
Qy	181	gValPheTyRHisIleSerPheGlySerArgIleProlGlyThrArgGlnArgAI	201			
Db	2955	ACAGGCCCTCATCTTCCGATCTTTATGCTCTAAACTGCGACGGTTGGCTAAATTATT	3014			
Qy	166	- - - - - GlutPheAlaGlyCysGlnArgValGlyIleSerProAspThrHisAR	181			
Db	3075	ACTCCCTATCACATCTCATTCATTCGGAATTCTCGGATTCTCAGCACCAGGCGCCAGGGTA	3134			
Db	3015	TCTCATCTTTAGGGCTGGATGAGGTAGATCTCCCGATACCCAGATCCACAG	3074			
Qy	201	a-----	201			
Db	3135	-GGTGGTATTCTGTCAAATACTTCAACTATTCAGTTGAAATACGGTTICAGATGA	3193			
Qy	201	- - - - -	201			
Db	3194	CCTGCCTTTAGGACACCCAGGGCCTGTTCTAGGAAGTTGGGAACCTGATAAGTAT	3255			
Qy	201	- - - - -	201			
Db	3254	ATCTAACTTAGGTAACCATATGACTCTAACATCTGCCTTATTCTGTGTTTACCT	3313			
Db	202	- - - - - ThrProAspIleProProAlaAspIeuGluAspPheLeuSerArgIlePheG1	219			
Db	3314	CAGGCCACCCAGATACCCCTCTGCTGATCTTCAGGATTCTTGTAGTCGGGATCTTCA	3373			
Qy	219	nValPheProGlyGlnNetProAsnGlyIleAsnPheAlaAlaProAlaProG1	239			
Db	3374	AGTACCCCAGGGAGTGCCTAATGGCAATTGCTGCTTCTGCTGCTGCTG	3433			
Qy	2295	CAAGCATTCTTATTAGAACGGAATGGAGAGAACGTGACTGCTCTGGACTGG	2234			
Db	72	- - - - -	72			
Qy	72	- - - - -	72			
Db	2235	GGCTCAAGGGCCAACTGATATGTCCTCCCTGAAATACCTTCTGACTTA	2294			
Qy	73	- - - - - LysArgMetAlaGluAsnIleLeuSerArgSerValAsn	85			
Db	2295	CAAGCATTCTTATTAGAACGGAATGGAGAGAACGTGACTGCTCTGGACTGG	2234			
Qy	86	GluPheLeuSerLysLeuGlnAspAspLeuLysGluAlaMetAsnThrMetMcSysSer	105			
Db	2355	GAGTTCTGTCACGCTCAAGCTGAAAGTACCTCAAGGGCAATGAAATACTAGATGTCAGC	2414			
Qy	239	YalaAlaAlaAlaSerLysProAsnSerThrValProLysGlyGluAlaLysProLySar	259			
Db	3434	ACCCGCTGCAAGCTCPAAGCCACAGCAACGAAACCTAACGGAAAGCTAACGG	3493			
Qy	259	QargLysLysValArgLysProPheGlnArg	269			
Db	3494	CCCCAC	3521			
Qy	106	ArgCysGlnGlyLysHis-----	111			

RESULT 1.0  
 AAC86936 standard; DNA; 12119 BP.  
 XX  
 AC AAC86936;  
 XX DT 02-APR-2001 (first entry)  
 XX DE Nucleotide sequence of a chimeric BVDV/HCV virus.  
 XX KW Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus;  
 HCV; vaccine; viral inhibitor; antiviral; ss.  
 OS Synthetic C.  
 OS Bovine viral diarrhoea virus.  
 OS Hepatitis C virus.  
 XX FH Key  
 FT Location/Qualifiers  
 PT 386..11893  
 FT /\*tag= a  
 XX PN WO200007352-A2.  
 XX PD 14-DEC-2000.  
 XX PP 02-JUN-2000; 2000WO-US15527.  
 XX PR 04-JUN-1999; 99US-0137817.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Nam J., Bukh J., Emerson SU., Purcell RH.  
 XX DR WPI; 2001-071081/08.  
 DR P-SDDB; AAB31167.  
 XX PS Disclosure; Page 62-66; 97pp; English.  
 XX The specification describes a nucleic acid comprising a chimeric virus genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the (non-)structural region has been replaced by the (non-)structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in screening for neutralizing antibodies to HCV of different genotypes, in the production of HCV-BVDV virions, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, in studying the molecular properties of HCV indirectly in vitro, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence represents a chimeric nucleic acid of the invention.  
 XX Sequence 12119 BP; 3589 A; 2668 C; 3211 G; 2651 T; 0 other;  
 SQ Alignment Scores:  
 Pred. No.: 5.446-33 Length: 12119  
 Score: 497.00 Matches: 89  
 Percent. Similarity: 98.90% Conservative: 1  
 Best Local Similarity: 97.80% Mismatches: 1  
 Query Match: 34.68% Indels: 0  
 DB: 22 Gaps: 0  
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 QY 103 MetCysSerArgCysGlnGlyLysHisArgArgPheGluMetAspArgGluProLySSer 122

Db 4535 ATGGCAGCCATGGCGAAACCTAAGGT 459.  
 QY 123 AlaArgTycysAlaGluGluLeuHisProAlaGluGluGlyAspPheTrpala 142  
 Db 4595 GCCGATACTGTGCTGAGTCATAAGGTCATCCTGAGGAAGGIGACTTTGGCA 4654  
 XX  
 YY 143 GluSerSerMetLeuGlyLeuLysIleThrPheAlaLeuMetAspGlyLysValTyr 162  
 DE 4655 GAGTGAGCATGTTGGCTCAAAATCACCTACTTGCTGATGCTGAAAGGTGAT 4714  
 XX  
 YY 163 AspIleIleGluLeuIlePheAlaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182  
 Db 4715 GATATCACAGACTGGCTGGATCTCCCAAGATACCCACAGAGTC 4774  
 XX  
 YY 183 ProTyrrHisIleSerPheGlySerArgIlePro 193  
 Db 4775 CCTTGTCACATCTCATTTGGTCAGGAGGCT 4807  
 RESULT 11  
 AA236196 standard; cDNA; 12578 BP.  
 ID AA236196  
 XX AC AA236196;  
 XX DT 11-FEB-2000 (first entry)  
 XX DE Nucleotide sequence of infectious BVDV NADL protein.  
 XX KW Psedorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
 KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
 KW bovine viral diarrhea virus; NADL; vaccine; ss.  
 XX  
 XX OS Bovine viral diarrhea virus.  
 XX FH Key  
 FT CDS 386..12352  
 FT /\*tag= a  
 /product= "NADL protein"  
 XX PN WO955366-A1.  
 XX PD 04-NOV-1999.  
 XX PF 23-APR-1999; 99WO-US08850.  
 XX PR 24-APR-1998; 98US-0082964.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PI Rice CM., Frolov I., McBride MS.;  
 XX DR WPI; 2000-013159/01.  
 DR P-PIDB; AAY55616.  
 XX PT Chimeric viral RNA, used in vaccine against BVDV -  
 XX PS Disclosure; Fig 11; 108p; English.  
 XX CC The present sequence encodes the NADL protein of bovine viral diarrhea virus (BVDV). The sequence is used in the course of the invention, to produce chimeric RNA viruses. The specification describes chimeric viral RNA comprising a 5' nontranslated region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where at least one of the regions is chimeric and comprises a nucleic acid sequence from a pestivirus in operable linkage with a heterologous nucleotide sequence, preferably from HCV. The chimeric viral RNA is replication-competent. The chimeric viral RNA can be used in a method for identifying compounds having antiviral activity against HCV. When the pestivirus viral nucleotide sequence is from bovine viral diarrhea virus (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV.  
 XX SQ Sequence 12578 BP; 4049 A; 2527 C; 3233 G; 2769 T; 0 other;

Alignment Scores:	5.69e-33	Length:	12578	CC	for screening compounds that inhibit HCV in vivo by inhibiting HCV
Pred. No.:	497.00	Matches:	89	CC	protease, where screening may be in cell culture or in an animal model.
Score:	98.90%	Conservative:	1	CC	The present sequence is a chimeric clone of BVDV (bovine viral diarrhea-virus)/HCV NS3-wt, which was used to illustrate the present invention.
Percent Similarity:	97.80%	Mismatches:	1	XX	
Best Local Similarity:	97.80%	Indels:	0	SQ	Sequence 12734 BP; 4032 A; 2604 C; 3295 G; 2803 T; 0 other;
Query Match:	34.68%	Gaps:	0		
DB:	21				
US-10-049-742-11 (1-269) × AAZ36196 (1-12578)					
Qy	103 MetCysSerArgCysGlnGlyLysIshisArgArgPheGluMetAspArgGluProlysSer 122	Alignment Scores:	5.78e-33	Length:	12734
Db	4994 ATGAGGCCATGCGAGGAAGCTAGGGTAAATGGACGGGAACTTAGAGT 5053	Pred. No.:	5.78e-33	Matches:	89
Qy	123 AlaArgTyrCysAlaGluCysAsnArgLeuHisProAlaGluGluglyAspPheTrpala 142	Score:	497.00	Conservative:	1
Db	5054 GCCAGATACTGTGCTAGTGTAAATGGCTGATCCGTGAGAACGTGACTTTGGCA 5113	Percent Similarity:	98.90%	Best Local Similarity:	1
Qy	143 GluSerSerMetLeuGlyLeuLysIleThrTyrPhAlaLeuMetAspArgLysValty 162	Query Match:	34.68%	Mismatches:	1
Db	5114 GAGTCAGGCTGTTGGCCCTAAATCACCPACTTGCGCTGATGGATGGAAAGGTGTAT 5173	DB:	24	Indels:	0
Qy	163 AspIleThrGluTrpalaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182			Gaps:	0
Db	5174 GATATCACAGTGTTGGGATCTCCAGATAACCACAGTC 5233				
Qy	183 ProTyRHisIleSerPheGlySerArgIlePro 193	US-10-049-742-11 (1-269) × ABAA95615 (1-12734)			
Db	5234 CCTTGTCACATCTCATTTGGTACCGATGCT 5266	Score:	103	MatCysSerArgCysGlnGlyLysIshisArgArgPheGluMetAspArgGluProlysSer 122	
RESULT 12		Percent Similarity:	98.90%	Best Local Similarity:	1
ABA95615		Query Match:	34.68%	Mismatches:	1
ID	ABA95615 standard; DNA; 12734 BP.	DB:	24	Indels:	0
XX		Gaps:	0	Gaps:	0
AC	ABA95615;				
XX					
DT	21-MAR-2002 (first entry)	RESULT 13			
XX		AAZ36203			
DE	Chimeric BVDV/HCV NS3-wt sequence.	ID	AAZ36203	standard; DNA; 12842 BP.	
KW	Pestivirus; Npro; protease; NS3; screening; ds.	XX	AAZ36203;		
XX		AC	AAZ36203;		
OS	Chimeric - Bovine viral diarrhea virus.	XX	AC		
OS	Chimeric - Hepatitis C virus.	XX	DT	11-FEB-2000 (first entry)	
XX		DE	DE	Nucleotide sequence of the prototype HCV-BVDV chimera.	
PN	US6326137-B1.	XX	KW	Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;	
XX	PD 04-DEC-2001.	XX	KW	5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;	
XX	Hong Z, Lai VCH, Lau JYN;	XX	KW	bovine viral diarrhea virus; NADL; vaccine; ss.	
PP	25-JUN-1999; 99US-0344456.	XX	OS	Chimeric - Hepatitis C virus.	
PP	25-JUN-1999; 99US-0344456.	XX	OS	Chimeric - Bovine viral diarrhea virus.	
PR	2002-121103/16.	XX	PN	WO995366-A1.	
XX	(SCHE ) SCHERING CORP.	XX	XX		
PA		PD	04-NOV-1999.		
XX		XX	XX		
PI	Hong Z, Lai VCH, Lau JYN;	PR	24-APR-1999;	98US-0082264.	
XX		XX	XX		
DR	WPI; 2002-121103/16.	PD	23-APR-1999;	99WO-US08850.	
XX		XX	XX		
PT	Nucleic acid construct encoding chimeric Hepatitis C Virus (HCV) pestivirus genome where the Npro protease gene is replaced with NS3 protease gene, useful for in vivo screening of compounds which inhibit HCV infection -	PI	PI	UNIV WASHINGTON.	
PT		Rice CM, Frolov I, McBride MS;	XX		
PT		XX	XX		
XX	Example 2: Columns 17-28; 20pp; English.	XX	XX	WPI; 2000-01335/01.	
CC	The present invention relates to a nucleic acid construct encoding a chimeric Hepatitis C virus (HCV)-pestivirus genome. The construct comprises a pestivirus genome where a Npro pestivirus protease gene is replaced with a gene encoding a functional HCV NS3 protease. Furthermore, each junction site recognised by the Npro protease is replaced with a junction site recognised by the HCV NS3 protease. The construct is useful	CC	XX	Chimeric viral RNA, used in vaccine against BYDV -	
CC		CC	XX	Example 5; Fig 19; 108pp; English.	
PS		PS	XX	The present sequence represents the prototype Hepatitis C virus	

CC (HCV)-bovine diarrheal virus (BVDV) chimeric virus of the invention. The sequence contains the adapted HCV 5'NTR from CC 5'NTR/R3orig and tandem 3'NTR elements from HCV followed by BVDV.  
 CC The specification describes chimeric viral RNA comprising a CC 5' nontranslated region (5'NTR); an open reading frame (ORF) region; CC and a 3' NTR; where at least one of the regions is chimeric and CC comprises a nucleotide sequence from a pestivirus in operable linkage CC with a heterologous nucleotide sequence, preferably from HCV. The CC chimeric viral RNA is replication-competent. The chimeric viral RNA CC can be used in a method for identifying compounds having antiviral activity against HCV. When the pestivirus viral nucleotide sequence is CC from bovine diarrhea virus (BVDV), the chimeric viral RNA can be CC used in a vaccine against BVDV.

XX Sequence 12842 BP; 4034 A; 2612 C; 3282 G; 2914 T; 0 other;

Alignment Scores:

Pred. No.: 5.84e-33 Length: 12842

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

US-10-049-742-11 (1-269) × AAZ36203 (1-12842)

Qy 103 MetCysSerArgCysGinGlyLysHisArgPheGluMetAspArgGluProLySer 122

Db 4962 ATGTGCAGCGATGCCGGAAAGCATGAGTTCAAATGACCGGAACTTANGAT 5021

Qy 123 AlaArgTyrCysAlaGluCysasnArgLeuHisProAlaGluGlyAspPheTrPAla 142

Db 5022 GCGAGATACTGTCGTGACTGTAAATGGTTGCACCCCTGGAAAGTGACTTTGGCA 5081

Qy 143 GluSerSerMetLeuGlyLeuLysIleThrTyrPheAlaLeuMetAspGlyLysValTyr 162

Db 5082 GAGTCGAGCATGTTGGCCCTCAAATCACCTACTTGGCTGATGGATGAAAGGTTA 5141

Qy 163 AspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182

Db 5142 GATATCACAGAGTGGCTGATGCCAGGTGAAATCTCCCAGATACCAAGAGTC 5201

Qy 183 ProTyRHisIleSerPheGlySerArgIlePro 193

Db 5202 CCTTGTCACATCTCATTTGGTCACGGSATGCGCT 5234

RESULT 14  
AAZ36211

ID AAZ36111 standard; DNA: 13198 BP.

XX AC AAZ36211;

XX DT 11-FEB-2000 (first entry)

DE Nucleotide sequence of functional HCV-BVDV chimera from PCBV/p7/IRES-pac.

XX KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;

KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;

KW bovine viral diarrhea virus; NADL; vaccine; ss.

XX Chimeric - Hepatitis C virus.

OS Chimeric - Bovine viral diarrhea virus.

XX PN WO995336-A1.

XX PD 04-Nov-1999.

XX PF 23-APR-1999; 99WO-US08850.

XX PR 24-APR-1998; 98US-0082964.

XX PA (UNIV ) UNIV WASHINGTON.

XX XX

RESULT 15  
AAA38807

ID AAA38807 standard; DNA: 14078 BP.

XX AC AAA38807;

XX DE 4329 CCTTGTCACATCTCATTTGGTCACGGATGCCT 4361

XX DT 31-AUG-2000 (first entry)

XX Bovine viral diarrhea virus; attenuation; Npro protease; enzyme;

KW mucosal disease; ulcer; enteric disease; pneumonia; BVDn1; antiviral;

XX diarrhoea; ds.

XX OS Bovine viral diarrhea virus.

XX Synthetic.

XX FH Key Location/Qualifiers

XX FT 39..12116

PI Rice CM, Frolov I, McBride MS;

XX XX WPI: 2000-013359/01.

XX PT Chimeric viral RNA, used in vaccine against BVDV

XX PS Example 3; FIG 24; 108PP; English.

XX The present sequence represents a functional Hepatitis C virus (HCV)-bovine viral diarrhea virus (BVDV) chimeric virus of the invention, expressing a dominant selectable marker conferring resistance to puromycin. The specification describes chimeric viral RNA comprising a 5', nontranslated region (5'NTR); an open reading frame (ORF) region;

CC and a 3' NTR; where at least one of the regions is chimeric and CC comprises a nucleotide sequence from a pestivirus in operable linkage CC with a heterologous nucleotide sequence, preferably from HCV. The CC chimeric viral RNA is replication-competent. The chimeric viral RNA CC can be used in a method for identifying compounds having antiviral CC activity against HCV. When the pestivirus viral nucleotide sequence is CC from bovine diarrhea virus (BVDV), the chimeric viral RNA can be CC used in a vaccine against BVDV.

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 5.84e-33 Length: 12842

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

XX SQ Sequence 13198 BP; 3735 A; 3097 C; 3533 G; 2833 T; 0 other;

XX Alignment Scores:  
Pred. No.: 6.04e-33 Length: 13198

Score: 497.00 Matches: 89

Percent Similarity: 98.90% Conservative: 1

Best Local Similarity: 97.80% Mismatches: 1

Query Match: 34.68% Indels: 0

DB: 21 Gaps: 0

Job time : 359 secs

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```

FT      /*tag= a
FT      /label= BVDDN1 genome
FT      /note= "BVDDN1 genome is claimed in Claim 1 of
FT      specification"
XX      EP1013757-A2.
XX      28-JUN-2000.
XX      PD
XX      08-NOV-1999; 99EP-0308866.
XX      PF 10-NOV-1998; 98US-0107908.
XX      (PFIZ ) PFIZER PROD INC.
XX      PA
XX      PI Cao X, Sheppard MG;
XX      DR; 2000-414600/36.
XX      Attenuated bovine viral diarrhea virus, used as a vaccine to give
PT      cattle protective immunity against subsequent infection with the virus
PT
XX      PS; Fig 2; 442P; English.
XX      Bovine viral diarrhea virus (BVVD) causes mucosal disease in infected
CC      cattle. Symptoms include elevated temperature, coughing, diarrhoea and
CC      ulceration of the alimentary mucosa. This virus can be transmitted via
CC      the placenta to unborn calves. These calves suffer from persistent
CC      infection and are highly predisposed to infection with microorganisms
CC      causing diseases such as pneumonia or enteric diseases. The present
CC      sequence is a plasmid which carries a mutated form of the bovine viral
CC      diarrhea virus (pBVDDN1). The mutated BVVD was produced by deleting the
CC      Npro Protease gene from the wild type viral genome. The Npro Gene
CC      functions in proteolytic cleavage. The mutated virus was found to be
CC      attenuated i.e. the virus replicates at a slower rate than the wild type
CC      virus and so is less infectious. The mutated virus is therefore suitable
CC      for use in vaccines for cattle.
XX      Sequence 14078 BP; 4407 A; 2901 C; 3608 G; 3162 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 6.55e-33 Length: 14078
Score: 497.00 Matches: 89
Percent Similarity: 98.90% Conservative: 1
Best Local Similarity: 97.80% Mismatches: 1
Query Match: 34.66% Indels: 0
DB: 21 Gaps: 0
US-10-049-742-11 (1-269) x AAA38807 (1-14078)
Qy 103 MetCysSerArgCysGlnGlyLysHisArgArgPheGluMetAspArgGluProLysSer 122
Db 4532 ATGGCGACGATGCCGGAAAGATGGAGGTGAAATGACCGGAACCTAGAT 4591
Qy 123 AlaArgTyrCysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspPheTrPAla 142
Db 4592 GCCAGATACTGTCGAGTAAATGGCTGCAATCTGAGAACTGACTTTGGCA 4651
Qy 143 GluSerSerMetLeuGlyLeuLysIleThrIleThrPheAlaLeuMetAspGlyIysValYr 162
Db 4652 GAGTCGAGCATGGTGGCCCTAAATTCACTTACGTTGCTGATGGATGAAAGGTGTA 4711
Qy 163 AspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182
Db 4712 GATATCACAGACTGGGTGGATGCCAACGTTGGATCTCCCCAGATAACCCACAGATC 4771
Qy 183 ProTyrosIleSerPheGlySerArgIlePro 193
Db 4772 CCTTGTCACATCTCATTTGTTACCGGATGGCT 4804

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GenCore version 5.1.6  
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DM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 1, 2003, 09:37:08 ; Search time 74 Seconds  
(Without alignments)  
1604.487 Million cell updates/sec

Title: US-10-049-742-11  
Perfect score: 1433  
Sequence: 1 MAGYPEDELNPFPVHLGVREAT.....VPKGBAKPCKRKVTRRPFQR 269

Scoring table: BJOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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DB=Issued\_Patents\_NA -QFM=Fasta -SUFFIX=rni -MINMATCH=0.1 -LOCFILE=0  
LOOPTIMEOUT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blocsum62 -TRANS=human40.cdi  
LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15.  
USER=US10049742 @CGN 1.1 .56 @runat\_01122003\_073137\_18627 -NCPU=6 -ICPU=3  
NO\_NMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
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FGAPEXT=7 -YGAPOP=10 -YGAPEXT=7 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMBO.seq;\*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMBO.seq;\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMBO.seq;\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

**SUMMARIES**

Result No.	Score	Match	Length	DB ID	Description
1	497	34.7	12734	4 US-09-344456-1	Sequence 1, Appli
2	497	34.7	14078	3 US-09-433262-1	Sequence 1, Appli
3	497	34.7	14078	4 US-09-702330-4	Sequence 1, Appli
4	497	34.7	14578	3 US-08-859694-1	Sequence 1, Appli
5	173.5	11.1	635	4 US-09-669751-166	Sequence 855, App
6	159	11.1	1128	4 US-09-328352-58	Sequence 165, App
7	156.5	10.9	2349	2 US-08-974546-2	Sequence 2, Appli
8	155.5	10.9	1376	3 US-09-235373-7	Sequence 2, Appli
9	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
10	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
11	155.5	10.9	1621	4 US-09-995243-147	Sequence 141, App
12	155	10.8	8050	3 US-09-4913362-11	Sequence 11, Appli

**SEQUENCES**

Result No.	Query	Match	Length	DB ID	Description
1	497	34.7	12734	4 US-09-344456-1	Sequence 1, Appli
2	497	34.7	14078	3 US-09-433262-1	Sequence 1, Appli
3	497	34.7	14078	4 US-09-702330-4	Sequence 1, Appli
4	497	34.7	14578	3 US-08-859694-1	Sequence 1, Appli
5	173.5	11.1	635	4 US-09-669751-166	Sequence 855, App
6	159	11.1	1128	4 US-09-328352-58	Sequence 165, App
7	156.5	10.9	2349	2 US-08-974546-2	Sequence 2, Appli
8	155.5	10.9	1376	3 US-09-235373-7	Sequence 2, Appli
9	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
10	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
11	155.5	10.9	1621	4 US-09-995243-147	Sequence 141, App
12	155	10.8	8050	3 US-09-4913362-11	Sequence 11, Appli

**ALIGNMENTS**

Result No.	Aligner	Score	Length	Start	End	Sequence
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4	US-09-370838-140	1881	3	140	144	Sequence 1, Appli
5	US-09-838165	1881	4	140	144	Sequence 1, Appli
6	US-09-613303-88	1881	4	140	144	Sequence 1, Appli
7	US-09-8402-11	1881	3	140	144	Sequence 1, Appli
8	US-09-103-8404-1	1881	3	140	144	Sequence 1, Appli
9	US-09-1129	1881	3	140	144	Sequence 1, Appli
10	US-09-149476-188	1881	4	140	144	Sequence 1, Appli
11	US-09-188165	1881	4	140	144	Sequence 1, Appli
12	US-09-4528D-1	1881	4	140	144	Sequence 1, Appli
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15	US-09-188165	1881	4	140	144	Sequence 1, Appli
16	US-09-252991A-10250	1881	4	140	144	Sequence 1, Appli
17	US-09-252991A-10250	1881	4	140	144	Sequence 1, Appli
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19	US-09-8402-11	1881	3	140	144	Sequence 1, Appli
20	US-09-149476-188	1881	4	140	144	Sequence 1, Appli
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22	US-09-838165	1881	4	140	144	Sequence 1, Appli
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26	US-09-1129	1881	3	140	144	Sequence 1, Appli
27	US-09-149476-188	1881	4	140	144	Sequence 1, Appli
28	US-09-188165	1881	4	140	144	Sequence 1, Appli
29	US-09-2528D-1	1881	4	140	144	Sequence 1, Appli
30	US-09-658644-3	1881	4	140	144	Sequence 1, Appli
31	US-09-8402-11	1881	3	140	144	Sequence 1, Appli
32	US-09-149476-188	1881	4	140	144	Sequence 1, Appli
33	US-09-328352-3811	1881	4	140	144	Sequence 1, Appli
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35	US-09-235373-4	1881	3	140	144	Sequence 1, Appli
36	US-09-388993-4	1881	3	140	144	Sequence 1, Appli
37	US-09-134-001C-851	1881	3	140	144	Sequence 1, Appli
38	US-09-486955A-6	1881	3	140	144	Sequence 1, Appli
39	US-09-557884-1	1881	3	140	144	Sequence 1, Appli
40	US-09-613300-1	1881	4	140	144	Sequence 1, Appli
41	US-09-620312D-820	1881	4	140	144	Sequence 1, Appli
42	US-09-996243-149	1881	4	140	144	Sequence 1, Appli
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45	US-08-961-527-189	1881	4	126.5	126.5	Sequence 4, Appli

**RESULTS**

Result No.	Score	Match	Length	DB ID	Description
1	497	34.7	12734	4 US-09-344456-1	Sequence 1, Appli
2	497	34.7	14078	3 US-09-433262-1	Sequence 1, Appli
3	497	34.7	14078	4 US-09-702330-4	Sequence 1, Appli
4	497	34.7	14578	3 US-08-859694-1	Sequence 1, Appli
5	173.5	11.1	635	4 US-09-669751-166	Sequence 855, App
6	159	11.1	1128	4 US-09-328352-58	Sequence 165, App
7	156.5	10.9	2349	2 US-08-974546-2	Sequence 2, Appli
8	155.5	10.9	1376	3 US-09-235373-7	Sequence 2, Appli
9	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
10	155.5	10.9	1376	3 US-09-388993-2	Sequence 2, Appli
11	155.5	10.9	1621	4 US-09-995243-147	Sequence 141, App
12	155	10.8	8050	3 US-09-4913362-11	Sequence 11, Appli

**GENERAL INFORMATION:**

- APPLICANT: Hong, Zhi
- APPLICANT: Lai, Vicki C.H.
- APPLICANT: Lau, Johnson Y.N.
- FILE REFERENCE: IN10138
- CURRENT APPLICATION NUMBER: US/09/344456A
- CURRENT FILING DATE: 1999-06-25
- NUMBER OF SEQ ID NO: 4
- SOFTWARE: PatentIn Ver. 2.1
- SEQ ID NO 1
- TYPE: DNA
- ORGANISM: Artificial Sequence
- FEATURE:
- OTHER INFORMATION: Description of Artificial Sequence: Chimeric
- OTHER INFORMATION: Pestivirus
- US-09-344456-1

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Pred. No.: 1 Score: 497.00  
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Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 2 Alignment Scores: 1.86E-37  
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Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 3 Alignment Scores: 1.86E-37  
Pred. No.: 3 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
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Pred. No.: 4 Score: 497.00  
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Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
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- Pred. No.: 8 Alignment Scores: 1.86E-37  
Pred. No.: 8 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
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- Pred. No.: 9 Alignment Scores: 1.86E-37  
Pred. No.: 9 Score: 497.00  
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DB: 4
- Pred. No.: 10 Alignment Scores: 1.86E-37  
Pred. No.: 10 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 11 Alignment Scores: 1.86E-37  
Pred. No.: 11 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 12 Alignment Scores: 1.86E-37  
Pred. No.: 12 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 13 Alignment Scores: 1.86E-37  
Pred. No.: 13 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 14 Alignment Scores: 1.86E-37  
Pred. No.: 14 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 15 Alignment Scores: 1.86E-37  
Pred. No.: 15 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 16 Alignment Scores: 1.86E-37  
Pred. No.: 16 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 17 Alignment Scores: 1.86E-37  
Pred. No.: 17 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 18 Alignment Scores: 1.86E-37  
Pred. No.: 18 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 19 Alignment Scores: 1.86E-37  
Pred. No.: 19 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 20 Alignment Scores: 1.86E-37  
Pred. No.: 20 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 21 Alignment Scores: 1.86E-37  
Pred. No.: 21 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 22 Alignment Scores: 1.86E-37  
Pred. No.: 22 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 23 Alignment Scores: 1.86E-37  
Pred. No.: 23 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 24 Alignment Scores: 1.86E-37  
Pred. No.: 24 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 25 Alignment Scores: 1.86E-37  
Pred. No.: 25 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 26 Alignment Scores: 1.86E-37  
Pred. No.: 26 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 27 Alignment Scores: 1.86E-37  
Pred. No.: 27 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 28 Alignment Scores: 1.86E-37  
Pred. No.: 28 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 29 Alignment Scores: 1.86E-37  
Pred. No.: 29 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 30 Alignment Scores: 1.86E-37  
Pred. No.: 30 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 31 Alignment Scores: 1.86E-37  
Pred. No.: 31 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 32 Alignment Scores: 1.86E-37  
Pred. No.: 32 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 33 Alignment Scores: 1.86E-37  
Pred. No.: 33 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 34 Alignment Scores: 1.86E-37  
Pred. No.: 34 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 35 Alignment Scores: 1.86E-37  
Pred. No.: 35 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 36 Alignment Scores: 1.86E-37  
Pred. No.: 36 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 37 Alignment Scores: 1.86E-37  
Pred. No.: 37 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 38 Alignment Scores: 1.86E-37  
Pred. No.: 38 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 39 Alignment Scores: 1.86E-37  
Pred. No.: 39 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 40 Alignment Scores: 1.86E-37  
Pred. No.: 40 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 41 Alignment Scores: 1.86E-37  
Pred. No.: 41 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 42 Alignment Scores: 1.86E-37  
Pred. No.: 42 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 43 Alignment Scores: 1.86E-37  
Pred. No.: 43 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 44 Alignment Scores: 1.86E-37  
Pred. No.: 44 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 45 Alignment Scores: 1.86E-37  
Pred. No.: 45 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 46 Alignment Scores: 1.86E-37  
Pred. No.: 46 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 47 Alignment Scores: 1.86E-37  
Pred. No.: 47 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 48 Alignment Scores: 1.86E-37  
Pred. No.: 48 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 49 Alignment Scores: 1.86E-37  
Pred. No.: 49 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 50 Alignment Scores: 1.86E-37  
Pred. No.: 50 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 51 Alignment Scores: 1.86E-37  
Pred. No.: 51 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 52 Alignment Scores: 1.86E-37  
Pred. No.: 52 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 53 Alignment Scores: 1.86E-37  
Pred. No.: 53 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 54 Alignment Scores: 1.86E-37  
Pred. No.: 54 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 55 Alignment Scores: 1.86E-37  
Pred. No.: 55 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 56 Alignment Scores: 1.86E-37  
Pred. No.: 56 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 57 Alignment Scores: 1.86E-37  
Pred. No.: 57 Score: 497.00  
Percent Similarity: 98.90%  
Best Local Similarity: 97.80%  
Query Match: 34.68%  
DB: 4
- Pred. No.: 58 Alignment Scores: 1.86E-37  
Pred. No.: 58 Score:

Db 5150 ATGGCAGCCATGCCAGGAAAGCATAGGGTTGAAATGGACGGGAACCTAAGAT 5209  
 Qy 123 Ala Arg Tyr Cys Asn Arg Leu His Pro Ala Glu Glu Gly Asp Phe Trp Ala 142  
 Db 5210 GCGAGATACTGGCTGCTAGTGTAAATGGCTGATCCCTGCAAGTGACTTGGCA 5269  
 Qy 143 Glu Ser Ser Met Leu Gly Lys Ile Thr Tyr Phe Ala Leu Met Asp Gly Lys Alanine 162  
 Db 5270 GAGTCGAGCATGGCCCTCAAATCACACTTGGCTGATGATGGAAAGGTGTAT 5329  
 Qy 163 Asp Ile Thr Glu Trp Ala Gly Cys Gln Arg Val Gly Ile Ser Pro Asp Thr His Arg Val 182  
 Db 5330 GATATCACAGACTGGGTGGATGCCACGGTGTGGGATCTCCCCAGATAACCCACAGAGTC 5389  
 Qy 183 Pro Ty R His Ile Ser Phe Gly Ser Arg Ile Pro 193  
 Db 5390 CCTTGTCACATCTCAATTGGTTCACGGATGCC 5422

RESULT 2

; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Xuemei  
 ; APPLICANT: Sheppard, Mike  
 ; TITLE OF INVENTION: ATTENUATED FORMS OF BOVINE VIRAL DIARRHEA VIRUS  
 ; FILE REFERENCE: PC10435A  
 ; CURRENT APPLICATION NUMBER: US/09/702,330  
 ; CURRENT FILING DATE: 2000-10-31  
 ; PRIOR APPLICATION NUMBER: 09/433,262  
 ; PRIOR FILING DATE: 1999-11-04  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 1  
 ; TYPE: DNA  
 ; ORGANISM: Bovine Viral Diarrhea Virus  
 ; US-09-702-330-1

Alignment Scores:  
 Pred. No.: 2.14e-37 Length: 14078  
 Score: 497.00 Matches: 89  
 Percent Similarity: 98.90% Conservative: 1  
 Best Local Similarity: 97.80% Mismatches: 1  
 Query Match: 34.68% Indels: 0  
 DB: 4  
 ; US-10-049-742-11 (1-269) x US-09-702-330-1 (1-14078)

Qy 103 Met Cys Ser Arg Cys Glu Gly Lys His Arg Arg Phe Glu Met Asp Arg Glu Pro Lys Ser 122  
 Db 4532 ATGTCGAGCCATGGCTGAGTGTAAATGGCTGATCCCTGCAAGTGACTTGGCA 4591  
 Qy 123 Ala Arg Tyr Cys Asn Arg Leu His Pro Ala Glu Glu Gly Asp Phe Trp Ala 142  
 Db 4592 GCCAGATACTGGCTGAGTGTAAATGGCTGATCCCTGCAAGTGACTTGGCA 4651  
 Qy 143 Glu Ser Ser Met Leu Gly Lys Ile Thr Tyr Phe Ala Leu Met Asp Gly Lys Alanine 162  
 Db 4652 GAGTCGAGCATGGCCCTCAAATCACACTTGGCTGATGGAAAGGTGTAT 4711  
 Qy 163 Asp Ile Thr Glu Trp Ala Gly Cys Gln Arg Val Gly Ile Ser Pro Asp Thr His Arg Val 182  
 Db 4712 GATATCACAGACTGGCTGATGGAAAGGTGTAT 4771  
 Qy 183 Pro Ty R His Ile Ser Phe Gly Ser Arg Ile Pro 193  
 Db 4772 CCTTGTCACATCTCAATTGGTTCACGGATGCC 4804

RESULT 4

US 08-859-694-1

Qy 103 Met Cys Ser Arg Cys Glu Gly Lys His Arg Arg Phe Glu Met Asp Arg Glu Pro Lys Ser 122  
 Db 4532 ATGTCGAGCCATGGCTGAGTGTAAATGGCTGATCCCTGCAAGTGACTTGGCA 4591  
 Qy 123 Ala Arg Tyr Cys Asn Arg Leu His Pro Ala Glu Glu Gly Asp Phe Trp Ala 142  
 Db 4592 GCCAGATACTGGCTGAGTGTAAATGGCTGATCCCTGCAAGTGACTTGGCA 4651  
 Qy 143 Glu Ser Ser Met Leu Gly Lys Ile Thr Tyr Phe Ala Leu Met Asp Gly Lys Alanine 162  
 Db 4652 GAGTCGAGCATGGCTGAGTGTAAATCACACTTGGCTGATGGAAAGGTGTAT 4711  
 Qy 163 Asp Ile Thr Glu Trp Ala Gly Cys Gln Arg Val Gly Ile Ser Pro Asp Thr His Arg Val 182  
 Db 4712 GATATCACAGACTGGCTGATGGAAAGGTGTAT 4771  
 Qy 183 Pro Ty R His Ile Ser Phe Gly Ser Arg Ile Pro 193  
 Db 4772 CCTTGTCACATCTCAATTGGTTCACGGATGCC 4804

US 08-859-694-1

Sequence 1, Application US/08859694A .  
 ; Patent No. 6001613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donis, Ruben O.  
 ; APPLICANT: Vassilev, Ventzislav B.  
 ; TITLE OF INVENTION: A plasmid bearing a cDNA copy of the genome of bovine viral diarrhea virus, chimeric derivations thereof, and method of producing an infectious bovine viral diarrhea virus using said plasmid  
 ; TITLE OF INVENTION: UNVN5110  
 ; FILE REFERENCE: UNVN5110  
 ; CURRENT APPLICATION NUMBER: US/08/859,694A  
 ; CURRENT FILING DATE: 1997-05-21  
 ; PRIOR APPLICATION NUMBER: 60/018,246  
 ; EARLIER FILING DATE: 1996-05-24  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 14578  
 ; TYPE: DNA  
 ; ORGANISM: bovine viral diarrhea virus  
 ; US-08-859-694-1

Alignment Scores:  
 Pred. No.: 2.24e-37 Length: 14578  
 ; Sequence 1, Application US/0970330 .  
 ; Patent No. 6410032

Score: 497.00 Matches: 99  
 Percent Similarity: 98.90% Conservative: 1  
 Best Local Similarity: 97.80% Mismatches: 1  
 Query Match: 34.68% Indels: 0  
 DB: 3 Gaps: 0

US-10-049-742-11 (1-269) x US-08-859-694-1 (1-14578)

Qy 103 MetCysSerArgCysGlnGlyLysHisIleArgArgPheGluMetAspArgGluProLySer 122  
 Db 5032 AtTCGACGCCATGCCAGGAAGCATAGGAGTTGAAATGACCGGAACTTAAGGT 5091

Qy 123 AlaArgTyrCysAlaGluCysSerArgLeuIleProAlaGluGluGlyAspPheTrpAla 142  
 Db 5092 GCGAGAATCTGCTGACTGTAAATAGGGTGCATCCTGTCAGCAAGGTGAC 5151

Qy 143 GluSerSerMetIleIleGlyLeuIysIleThrPheAlaLeuMetAspGlyLysValTyR 162  
 Db 5152 GAGTCGAGCAGTGGGCTCAAATACCTATTGGCTGAGTGGATGGAAAGGGTAT 5211

Qy 163 AspIlePheGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182  
 Db 5212 GATAATCACAGATGGCTGGATGCCAGGTGTGGAAATCTCCCCAGATAACCACAGTC 5271

Qy 183 ProTyRHisIleSerPhgGlySerArgIlePro 193  
 Db 5272 CCTTGTCACATCTCATTTGGTCACGGATGGCT 5304

RESULT 5

; Sequence 858, Application US/09328352  
 ; Patent No. 65622958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; TITLE OF INVENTION: BUCHANANI FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: GT099-01PA  
 ; CURRENT APPLICATION NUMBER: US/09/328-352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 858  
 ; LENGTH: 1128  
 ; TYPE: DNA  
 ; ORGANISM: Acinetobacter baumannii  
 ; FEATURE: unsure  
 ; NAME/KEY: unsure  
 ; LOCATION: (65)  
 ; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno

US-09-328-352-858

Alignment Scores:  
 Pred. No.: 9.67e-08 Length: 1128  
 Score: 173.50 Matches: 63  
 Percent Similarity: 36.02% Conservative: 34  
 Best Local Similarity: 24.14% Mismatches: 84  
 Query Match: 12.11% Indels: 83  
 DB: 4 Gaps: 11

US-10-049-742-11 (1-269) x US-09-328-352-858 (1-1128)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuIysAlaTyRArg 31  
 Db 34 TatGAGGTTCATGGCTTCAAAACCGCAAGTGTATGAGATCAAAAGCTATCGT 93

Qy 32 GlnLeuAlaValMetValHisPheAspLysAsn--HisIleProAlaIgluGluAla 50  
 Db 94 AAATTGGCGATGAAATATCATCTGACAGAAACCTGACATGCCGAGGTCAAAGAAA 153

Qy 51 PheLysValLeuDargAlaAlaTyrPaspIleValserAsnAlaIgluIysArgLysGluTyR 70  
 Db 154 TTAAAGAACGGCTTCGAGCTPATGAGATTTAGCTGACAGGAAAAACGACCATGAT 213

Qy 71 GluMerIysArgMerAlaGluIysArgLysGluIusUserArg--

RESULT 6

; Sequence 858, Application US/09328352  
 ; Patent No. 6551575  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Greenspan, Ralph J.  
 ; TITLE OF INVENTION: Methods for Identifying Compounds for Motion Sickness, Vertigo and Other Disorders Related to Acinetobacter  
 ; TITLE OF INVENTION: Balance, Motion Sickness, Vertigo and Other Disorders Related to Gravity  
 ; TITLE OF INVENTION: Methods for Identifying Compounds for Motion Sickness, Vertigo and Other Disorders Related to Acinetobacter  
 ; FILE REFERENCE: P-NI 3864  
 ; CURRENT APPLICATION NUMBER: US/09/669/151  
 ; CURRENT FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/168,579  
 ; PRIOR FILING DATE: 1999-12-02  
 ; NUMBER OF SEQ ID NOS: 261  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO 166  
 ; LENGTH: 635  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila  
 ; US-09-669-751-166

Alignment Scores:  
 Pred. No.: 1.09e-06 Length: 635  
 Score: 159.00 Matches: 29  
 Percent Similarity: 75.00% Conservative: 16  
 Best Local Similarity: 48.33% Mismatches: 15  
 Query Match: 11.10% Indels: 0  
 Gaps: 4

US-10-049-742-11 (1-269) x US-09-669-751-166 (1-635)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysLysAlaTyrArg 31  
 Db 186 TACAAGATTCTGGCCTGAGCGAAGCCAGGCACGGCATAGAAGGCC 245

Qy 32 GlnLeuAlaValMetValHisProAlpLysAsnGluAlaPhe 51  
 Db 246 AAACATGGCACCTCAAATACCATCCGAAGAACAAAGCAACAGCGGAGGCCCTC 305

Qy 52 LysValLeuAlaGluAlaLysAlaTrpAspIleValSerAsnAlaGluLysGlu 71  
 Db 237 AAGGAATTGGAGGGCTATAGTGCTAATGTGCTTAAGTGGCTGTATGAC 296

Qy 72 MetLysArgMetAlaGluAsnGluLeu 80  
 Db 297 ---CAGATGGGAGGAAGGGCTGAAGACGGGGTCACATGGTGCTCCCTCTTTGGT 350

RESULT 7  
 ; Sequence 2, Application US/08974546  
 ; Patent No. 5945287

; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Shah, Purvi  
 ; TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 6  
 ; CURRENT ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/974,546  
 ; FILING DATE: Filed Herewith  
 ; PRIOR APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0428  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEX/FAX: 650-845-166  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2349 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: BRAUTU21  
 ; CLONE: 2525691

US-09-974-546-2

Alignment Scores:  
 Pred. No.: 1.15e-05  
 Score: 156.50  
 Percent Similarity: 38.61%  
 Best Local Similarity: 25.49%  
 Query Match: 10.92%  
 DB: 2

US-10-049-742-11 (1-269) x US-08-974-546-2 (1-2349)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysLysAlaTyrArg 31  
 Qy 32 GlnLeuAlaValMetValHisProAlpLysAsnGluAlaPhe 51  
 Db 177 AAGATGGCCTGAGTACCCAGCAAGATAAAAGAACCCAAACGTGAGGAAGCTT 236

Qy 52 LysValLeuAlaGluAlaLysAlaTrpAspIleValSerAsnAlaGluLysGlu 71  
 Db 237 AAGGAATTGGAGGGCTATAGTGCTAATGTGCTTAAGTGGCTGTATGAC 296

Qy 72 MetLysArgMetAlaGluAsnGluLeu 80  
 Db 297 ---CAGATGGGAGGAAGGGCTGAAGACGGGGTCACATGGTGCTCCCTCTTTGGT 410

Db 351 GGCTCCCTTCACTACCCATGGGACCCCAGGCCACCTTGGCTCTTCTTGGT 410

Qy 81 -----SeArgSerValAlaGluPheLeuSer 89  
 Db 411 GGCTCCAAACCCCTTCGATATCTCTTGCCACGGGGCTCCACTGGCCCTCAGTGCGC 470

Qy 90 LysLeuGlnAspLeu 96  
 Db 471 TTGACCCAGATGACTGGATGTTGGATGAAATGAGGACCCATTGGCGCTTTCGGCGGT 530

Qy 97 GluAlaMetAsnThrMetMetCysSerArg-CysGlnGlyLys---HisArgArgPheG1 115  
 Db 531 TTGGGCTCAATGGCTG-----AGTAGGGCTCAAGGGCCAGAACCACTGTAC 584

Qy 115 uMetAspArgGluProLysSerAlaArgTyrCysAlaGluCysAsnArgLeuHisProAl 135  
 Db 585 CCTCGGCCAAGGTGCAAGGACCCCCAGTGGTCACAGCTGC----- 627

Qy 135 aGluGluGlyAspPheTrpAlaGluUserMet-LeuGlyLeuLysIleThrPheA 155  
 Db 628 -----GGGTGCTCCCTGGAGGAGRTRTACCATGGCTC-----CACCAAG 665

Qy 155 lLeuMetAspGlyLysValtyrAspIleThrGluLrpAlaGlyCysGlnArgValGlyI 175  
 Db 666 CCCATGAGATCACAGGGTGCCTAACCTGATGGGGAACGTGTGGCACCGAGAC 725

RESULT 8  
 US-08-868-288A-2  
 ; Sequence 2, Application US/08868288A  
 ; Patent No. 5932567  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: Bandman, Olga  
 ; CLONE: 2525691  
 ; TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/868,288A  
 FILING DATE: June 3, 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0309 US  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 415-855-0555  
 TELEPHONE: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1376 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: SYNORAB01  
 CLONE: 136466  
 US-08-868-288A-2

Alignment Scores:  
 Pred. No.: 6.89e-06 Length: 1376  
 Score: 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysAlaTyrArg 31  
 Percent Similarity: 80.33% Matches: 29  
 Best Local Similarity: 47.54% Conservative: 20  
 Query Match: 10.85% Mismatches: 11  
 DB: 2 DB: 1 Indels: 1  
 Gaps: 1

US-10-049-742-11 (1-269) × US-08-868-288A-2 (1-1376)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysAlaTyrArg 31  
 Db 274 TATAAAATCTTGGGGTCCTGCAGCTCATTAAGGATATTAAAGGCTTATAGGCTTATAGG 333

Qy 32 GlnLeuAlaAlaMetValHisProAspLysAsn--HisHisProArgAlaGluGluAla 50  
 Db 334 AACTAGCCCTGAGCTTATCCGACGGAACTCTGATGATCAAGGCCAGGAA 393

Qy 51 PheLysValLeuArgAlaAlaIleTrpAspIleValSerAsnAlaGluLysArgLysGluTyr 70  
 Db 394 TTCCAGGATCTGGTGTCTATGAGTTCTGTACATGTGAGAAACGGAAACGATAC 453

Qy 71 Glu 71  
 Db 454 GAT 456

RESULT 9

US-09-235-373-2  
 ; Sequence 2, Application US/09235373  
 ; Patent No. 6,001598  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Bandman, Olga  
 ; TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/235,373

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/868,288  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE DOCKET NUMBER: PF-0309 US  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1376 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: SYNOBAB01  
 CLONE: 136466  
 US-09-388-993-2

Alignment Scores:  
 Pred. No.: 6.89e-06 Length: 1376  
 Score: 155.50 Matches: 29  
 Percent Similarity: 80.33% Conservative: 20  
 Best Local Similarity: 47.54% Mismatches: 11  
 Query Match: 10.85% Indels: 1  
 DB: 3

US-10-049-742-11 (1-269) × US-09-388-993-2 (1-1376)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysAlaTyrG 31  
 ::|:|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 274 TATAAGATCTGGGGTGCCTGAAAGTCCTATAAGGATTTAAAAGGCCATAGG 333  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 32 GinLeuAlaValMetValHisProAspLysAsn--HisHisProArgAlaGluGluAla 50  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 334 AAATAGCTCTGGCTGACTCATCCGACCGAACCTGATGATCCACAGCCAGGAGAA 393  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 51 PheLysValLeuArgAlaAlaAlaPaspDipeptSerAsnAlaGluLysGlnGlnY 70  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 394 TTCCAGGATCTGGGTGCTPATGAGTTCTTCAGATGAGAAGCGAAACGAAACACTC 453  
 ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 71 Glu 71  
 ::|:  
 Db 454 GAT 456

RESULT 11  
 US-09-996-243-147  
 / Sequence 147, Application US/09996243  
 / Patent No. 6478825  
 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, HansPeter  
 / APPLICANT: Gerritsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Klijavin, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; ACIDS Encoding the Same  
 ; FILE REFERENCE: P2730P1C13  
 ; CURRENT APPLICATION NUMBER: US/09/996,243  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065185  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/087106  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087609  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087827  
 ; PRIOR FILING DATE: 1998-06-03  
 ; PRIOR APPLICATION NUMBER: 60/088021  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088025  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088026  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088028  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088029  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088030  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088033  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088326  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088167  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088222  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088212  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088217  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088655  
 ; PRIOR FILING DATE: 1998-06-09  
 ; PRIOR APPLICATION NUMBER: 60/088734  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088738  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088742  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088810  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088824  
 ; PRIOR APPLICATION NUMBER: 60/088826

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; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090698
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 8.63e-06 Length: 1621
Score: 155.50 Matches: 29
Percent Similarity: 80.33% Conservative: 20
Best Local Similarity: 47.54% Mismatches: 11
Query Match: 10.85% Indels: 1
DB: 4 Gaps: 1

US-10-049-742-11 (1-269) x US-09-996-243-147 (1-1621)

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysLysAlaArg 31
Db 237 TATAAGATCTGGGTCTGAAAGTCCTCTATAAAGGATAATTAAAAGCCCTATAGG 296
Qy 32 GlnLeuAlaValMetValHisProAspLysAsn--HisHisProArgAlaGluGluAla 50
Db 297 AAATGCCCCGAGCTCATGCCAGCGAACCTGTATGATGATGATGATGATGATGATG 356
Qy 51 PhoLysValLeuArgAlaAlaTrpAspIleValSerAsnAlaGluLysArgLysGluTyr 70
Db 357 TTCCAGGATCTGGGTCTGCCTATGAGGTTCTGTCAAGTAGTGAATGAGGAAACAGTAC 416

RESULT 12
US-09-491-162-11
Sequence 11, Application US/09491362
; Patent No. 6281017
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lange, Bernd M
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: WSUR14977
; CURRENT APPLICATION NUMBER: US/09/491,362
; CURRENT FILING DATE: 2000-01-26
; EARLIER APPLICATION NUMBER: 60/118,349
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentInventor Ver. 2.0

; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25

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SEQ ID NO: 11  
; LENGTH: 8050  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-491-362-11

Alignment Scores:  
Pred. No.: 8.76e-05 Length: 8050  
Score: 155.00 Matches: 61  
Percent Similarity: 38.61% Conservative: 39  
Best Local Similarity: 23.55% Mismatches: 92  
Query Match: 10.82% Indels: 68  
DB: 3 Gaps: 9

US-10-049-742-11 (1-269) x US-09-491-362-11 (1-8050)

Qy 6 GluAspGluLeuAsnProPheHisValLeuGlyAlaGluAlaSerAspValGlu 25  
Db 1061 GAAGGGAAATGAGCTTGTAGTCATGATCCCTTTAGCTTGATGATAAACA 1120

Qy 26 LeuLysLysAlaTyrArgGlnLeuAlaValMetValHisProAspLysAsnHiShiSPro 45  
Db 1121 GTGAAAGAACATTACAGAACCTTAGCTGCTGCTCACCGGACAGAACAGGTTAA 1180

Qy 46 ArgAlaGluGluAlaPheLeuAsnAlaGlu 65  
Db 1181 GGTGCCGAAGTGGCTTAACCTGGTTAGCTGGTTAGCTGCTACTATGATAAAGCT 1240

Qy 66 LysArgLysGlutYrGluMetLysArg-----MetAlaGluAsnGluLeuSerArg 82  
Db 1241 AAGAGATTGC-GTTGATCAAAGAGAAAACCAAGAAAAGGGGAAACCATGCTGCT 1299

Qy 83 SerValAsnGluPheLeuSerLysLeuGluAspAspLeuLysGluAlaMetAsn---- 100  
Db 1300 TCGTGTAAATAGGCTGAGGCCCTGCTCGTGAACCGGGGACATGACC 1359

Qy 101 -----ThrMetMetCysSerIleSerGlyCysGlnGlyLysHiSArg 112  
Db 1360 TTTCGACAGTCAGCATGACCTTTGACAGATGAATATGCAAAAGAGATGTTG 1419

Qy 113 ArgPheGluMetAspArgGluProLysserAlaArgCysAlaGluCysAsnArgLeu 132  
Db 1420 CATTTCGAGCAGATCATCTTAAAGACCTTCTCTCCAAACTCTGGTCAAG--- 1476

Qy 133 HisProAlaGluGluGlyAspPheTrpAlaGluSerSerMetLeuLysIleThr 152  
Db 1477 -----AATTGGCTATGACCAATAATCATGACA 1506

Qy 153 TyrPheAlaLeuMetAspGlyLysValtyrAspIleThrGluTrpAlaGlyCysGlnArg 172  
Db 1507 -----GAGGTGATCATGGAGGACAT-----ATCAGA 1536

Qy 173 ValGlyIleSerProAspThrHisArgValProTyrrHisIleSerPheGlySerArgIle 192  
Db 1537 GTCTCGTTCTCCGAAACAGAAAGAA-----CATCGGGCC 1575

Qy 193 ProGlyThrArgGlyArgGlnArgAlaThr-----ProAspAlaProAlaAspLeu 210  
Db 1576 ATTCTCAAGCAACTAGAGCAACTAGAGCTAGCATGCTATGATGCAAACTCTACTGAG-- 1632

Qy 211 GlnAspPheLeuSerArgIlePheGinValProProGlyGinMetProAsnGly/AsnPhe 230  
Db 1633 -----AGTTT 1638

Qy 231 PheAlaAlaProGlnProAlaProGlyAlaAlaAlaSerLysProAlaSerThr 249  
Db 1639 TTCAAGAAACCAATGCCGAAACAGGAGARGCA-----ACTCTACT 1680

RESULT 13  
US-09-874-562-11  
; Sequence 11, Application US/09874562  
; Patent No. 6420159  
; GENERAL INFORMATION:

; APPLICANT: Croteau, Rodney B  
; APPLICANT: Lange, Bernd M  
; TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND  
; TITLE OF INVENTION: METROBOLIC USE  
; FILE REFERENCE: WSUR17549  
; CURRENT APPLICATION NUMBER: US/09/874,562  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 09/491,362  
; PRIOR FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: 60/118,349  
; PRIOR FILING DATE: 1999-02-03  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 11  
; LENGTH: 8050  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-874-562-11

Alignment Scores:  
Pred. No.: 8.76e-05 Length: 8050  
Score: 155.00 Matches: 61  
Percent Similarity: 38.61% Conservative: 39  
Best Local Similarity: 23.55% Mismatches: 92  
Query Match: 10.82% Indels: 68  
DB: 4 Gaps: 9

US-10-049-742-11 (1-269) x US-09-874-562-11 (1-8050)

Qy 6 GluAspGluLeuAsnProPheHisValLeuGlyAlaGluAlaSerAspValGlu 25  
Db 1061 GAAGGGAAATGAGCTTGTAGTCATGATCCCTTTAGCTTGATGATAAACA 1120

Qy 26 LeuLysLysAlaTyrArgGlnLeuAlaValMetValHisProAspLysAsnHiShiSPro 45  
Db 1121 GTGAAAGAACATTACAGAACCTTAGCTGCTGCTCACCGGACAGAACAGGTTAA 1180

Qy 46 ArgAlaGluGluAlaPheLeuAsnAlaGlu 65  
Db 1181 GGTGCCGAAGTGGCTTAACCTGGTTAGCTGGCTCTACTATGCTGATAAAGCT 1240

Qy 66 LysArgLysGlutYrGluMetLysArg-----MetAlaGluAsnGluLeuSerArg 82  
Db 1241 AAGAGATTGC-GTTGATCAAAGAGAAAACCAAGAAAAGGGGAAACCATGCTGCT 1299

Qy 83 SerValAsnGluPheLeuSerLysLeuGluAspAspLeuLysGluAlaMetAsn---- 100  
Db 1300 TCGTGTAAATAGGCTGAGGCCCTGCTCGTGAACCGGGACATGACC 1359

Qy 101 -----ThrMetMetCysSerIleSerGlyCysGlnGlyLysHiSArg 112  
Db 1360 TTTCGACAGTCAGCATGACCTTTGACAGATGAATATGCAAAAGAGATGTTG 1419

Qy 113 ArgPheGluMetAspArgGluProLysserAlaArgCysAlaGluCysAsnArgLeu 132  
Db 1420 CATTTCGAGCAGATCATCTTAAAGACCTTCTCTCCAAACTCTGGTCAAG--- 1476

Qy 133 HisProAlaGluGluGlyAspPheTrpAlaGluSerSerMetLeuLysIleThr 152  
Db 1477 -----AATTGGCTATGACCAATAATCATGACA 1506

Qy 153 TyrPheAlaLeuMetAspGlyLysValtyrAspIleThrGluTrpAlaGlyCysGlnArg 172  
Db 1507 -----GAGGTGATCATGGAGGACAT-----ATCAGA 1536

Qy 173 ValGlyIleSerProAspThrHisArgValProTyrrHisIleSerPheGlySerArgIle 192  
Db 1537 GTCTCGTTCTCCGAAACAGAAAGAA-----CATCGGGCC 1575

Qy 193 ProGlyThrArgGlyArgGlnArgAlaThr-----ProAspAlaProAlaAspLeu 210  
Db 1576 ATTCTCAAGCAACTAGAGCAACTAGCTAGCATGCTATGACAACTCTACTGAG-- 1632

Qy 211 GlnAspPheLeuSerArgIlePheGinValProProGlyGinMetProAsnGly/AsnPhe 230  
Db 1633 -----AGTTT 1638

Qy 231 PheAlaAlaProGlnProAlaProGlyAlaAlaAlaSerLysProAlaSerThr 249  
Db 1639 TTCAAGAAACCAATGCCGAAACAGGAGARGCA-----ACTCTACT 1680

Qy 173 ValGlyIleSerProAspThrHisArgValProTyrrHisIleSerPheGlySerArgIle 192  
Db 1507 -----GAGGTGATCATGGAGGACAT-----ATCAGA 1536

Qy 193 ProGlyThrArgGlyArgGlnArgAlaThr-----ProAspAlaProAlaAspLeu 210  
Db 1537 GTCTCGTTCTCCGAAACAGAAAGAA-----ACTCTACT 1632

Qy 211 GlnAspPheLeuSerArgIlePheGlnValProProGlyInMetProAsnGlyAsnPhe 230  
 Db 1633 -----AGTTTT 1638  
 Qy 231 PheAlaAlaProGlyAlaAlaAlaAlaSerLysProAlaSerThr 249  
 Db 1639 TTCAAGAACAAATGCCAACACAGGAGATGCA-----ACTCTACT 1680  
**RESULT 14**  
 US-09-103-840A-2/C  
 ; Sequence 2, Application US/09103840A  
 ; Patent No. 6294328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: FRASER, Claire M.  
 ; APPLICANT: VENTER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; FILE REFERENCE: 24366-20007-0  
 ; CURRENT APPLICATION NUMBER: US/09/103, 840A  
 ; CURRENT FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 4403765  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; FEATURE:  
 ; OTHER INFORMATION: CDC 1551  
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
 ; OTHER INFORMATION: represent a, t, c or g  
 ; US-09-103-840A-2

Alignment Scores:  
 Pred. No.: 0.897 Length: 4403765  
 Score: 152.50 Matches: 79  
 Percent Similarity: 30.54% Conservative: 45  
 Best Local Similarity: 19.46% Mismatches: 100  
 Query Match: 10.64% Indels: 183  
 DB: 3 14 Gaps: 14

US-10-049-742-11 (1-269) x US-09-103-840A-2 (1-4403765)

Qy 12 PheIleValValGluAlaIleSerAspValGluLeuLysAlaItyArg 31  
 Db 2651266 TACGGGTGTCGGTGAAGCAGCGAACGTCATCAAACGGCCATCCGC 2651207  
 Qy 32 GlnLeuAlaValMetValHisProAspLysAsnHisHisProArgAlaGluAlaPhe 51  
 Db 2651206 AAGCTGCAGCTGGCTACAGGTGCAATCCGAGTCACCCGACAGGCTGGCAACATTGCA 2651147  
 Qy 52 LysValLeuArgAlaAlaIleAspIleValSerAsnAlaGluLysArgLysGluTyRglu 71  
 Db 2651146 AAAGAAATCAGGTCGCTACAGGTGCAATCCGAGTCACCCGACAGGCTGGCAACATTGCA 2651087  
 Qy 72 MetLysArgMetAlaGluAsnGluLeuSerArgSerValAsnGluPhe- 87  
 Db 2651086 CTGGCCGGATCGCTGGAGAGCCGGCTGCGGCCGCAATGGTTCGTTGGC 2651027  
 Qy 87 -----  
 Db 2651026 GCCCTCGGGAGCTGGCTGGAGGTTCTTGGCGGGGTTGGACTGGCTACAAATGGCTGGAT 2650967  
 Qy 88 -----LeuSerLysLeuGlnAspAsp 94  
 Db 2650966 CGAGGGCGATCGGCCGGTCCGGCGGGTTGGACTGGCTACAAATGGCTGGAT 2650907  
 Qy 95 LeuLysGlnAlaMet-----AsnThrMetMetCys 104  
 Db 2650906 CTCGAAAGTAGGCGAACAGGTGTCACCAAGCAGGTACCGTCGATAACCGCGTGTGCG 2650847  
 Qy 105 SerArgCysGlnGlyLysHisIleArg----- 112

; LENGTH: 4411529

Db 2650846 GACCGGTGCGAGGGACCAACAGGGGATTCGGATACCCCTGGGACACCTGC 2650787  
 Qy 113 -----ArgPheGluMetAspArgGluProLysSe----- 123  
 Db 2650786 GTGGCGGCGGGAGGTGAGCACCGTGAGCTGTTGGCTAGATGTTGACGATCCCTGTTGGCTG 2650727  
 Qy 124 ArgTyrcysAlaGluCys----- 129  
 Db 2650726 CGGCCGTGTCACCTGCCGGCTGGCTGGGTTATCCCGACCCGGTCCAGGATGC 2650667  
 Qy 130 -----AsnArgLeuHisProAlaGluLys----- 137  
 Db 2650666 ATGGGGATGCGGATGCGAATTCGGGGCTGGGGAGGAGATAGCCTCAAGATCCCSCCGCTGTC 2650607  
 Qy 137 ----- 137  
 Db 2650606 GCGGACGGATGCGAATTCGGCTCGGGCTAGGGAGGCTGGGGAGGGCG 2650547  
 Qy 138 ---G1-AspPheTrpAlaGlu----- 143  
 Db 2650546 GCGGGTGACCTCTACTGAGTCATGAGCAGGCCCCACGAGTCTTGTCCGGAGGTT 2650487  
 Qy 144 -----SerSerMetLeuGlyLeuLysIle 151  
 Db 2650486 GACCATCTGATTTGCAAGGTTTCGGGCCATGGTACGCGGCCAGGGTTAACGTC 2650427  
 Qy 152 ThrTyrPheAlaLeuMetAspGlyLysValtryAspIleThrGluLrpAlaGlyCysGln 171  
 Db 2650426 ACGGTGAGGCCATCTGGAC----- 2650406  
 Qy 172 ArgValGlyIleSerProAspThrHisArgValProTyRHisLysSerPheGlySerArg 191  
 Db 2650405 -----GGCTAGCGA-GATCACCATTCACCCGGCACGAGCCAGGTTCGGTGTAC 2650353  
 Qy 192 IleProGlyThrArgGlyArgGlnArgAlaThrProAspAlaProProAlaAspLeuGln 211  
 Db 2650152 GCTGGCGGTGAGG----- 2650323  
 Qy 212 AspPheLeuSerArgIlePheGlnValPro----- 229  
 Db 2650322 -----TTCCAACACGGCTGGCACGTTACAGTGGAGGT----- 2650284  
 Qy 230 PhePheAlaAlaProGlnProAla----- 243  
 Db 2650283 -----GGTGGCCTCCGACCCGCTGGATCAGGACATCGAACCTGCG 2650230  
 Qy 244 SerLysProAsnSerThrValProLysGlyGluAlaLysProLysArgArgLysSval 263  
 Db 2650229 GGGTCGCGCGACCCGCTGGTCCGGTGAACCCACGCGCCGGGACT 2650170

RESULT 15  
 US-09-103-840A-1/C  
 ; Sequence 1, Application US/09103840A  
 ; Patent No. 6294328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: FRASER, Claire M.  
 ; APPLICANT: VENTER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; TITLE OF INVENTION: TUBERCULOSIS  
 ; FILE REFERENCE: 24366-20007-0  
 ; CURRENT APPLICATION NUMBER: US/09/103, 840A  
 ; CURRENT FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 1  
 ; LENGTH: 4411529

TYPE: DNA  
 ORGANISM: Mycobacterium tuberculosis  
 OTHER INFORMATION: H37Rv  
 US-09-103-840A-1

**Alignment Scores:**  
 Pred. No.: 0.899  
 Score: 152.50  
 Percent Similarity: 30.54%  
 Best Local Similarity: 19.46%  
 Query Match: 10.64%  
 DB: 3

US-10-049-742-11 (1-269) × US-09-103-840A-1 (1-4411529)

Qy 12 PheHisValLeuGlyvalGluAlaThrAlaSerAspValGluLeuLysLysAlaTyrArg 31  
 Score: 45  
 保守性: 45  
 暂差错: 100  
 缺失: 183  
 插入: 14  
 DB: 2653970 TAGGGCTGTCTGGCTGTAGCAGAACCCGAAATCAACAGCCCTACCG 2653911

Qy 32 GlnLeuAlaValMetValHisProAspLysAsnHiShiProArgAlaGluGluAlaPhe 51  
 Score: 45  
 保守性: 45  
 暂差错: 100  
 缺失: 183  
 插入: 14  
 DB: 2653910 AAGCTGCGCAGCTGATCCGAGCTCAACCCGACGAGCTGCAGCAAATTC 2653851

Qy 52 LysValLeuArgAlaAlaAlaLeuValSerAsnAlaGluLysArgLysGluTyrGlu 71  
 Score: 45  
 保守性: 45  
 暂差错: 100  
 缺失: 183  
 插入: 14  
 DB: 2653850 AAAAGAAATCAGGGCTCGCTACTAGGGTCTCATGACCCGACAACGTCATCGCAG 2653791

Qy 72 MetLysArgMetAlaGluAsnGluLeuSerArgSerValAspGluPhe----- 87  
 Score: 45  
 保守性: 45  
 暂差错: 100  
 缺失: 183  
 插入: 14  
 DB: 2653790 CTGGGCCGGGATCCGGTGGAGGCCGCTGGGGCGCAATGGGTTGGCTGGC 2653731

Qy 87 ----- 87

DB: 2653730 GGCCCTGGCGAGGGTTCAGGGGTTCTTGGGGGGTTGGTGGGGGGCGGCTTC 2653671

Qy 88 ----- 87

DB: 2653670 CGAGGGCCGATGGCCGGTCCGGGTTTCAGGGGTTGGACTTCGCTGCTACGAATGGGCTGGAT 2653611

Qy 95 LeuLysGluAlaMet ----- 104

DB: 2653610 CTCGARGAGTGGCCACAGGGTCAACAGGGTCAACGGGTACCGTGATACCCTGGGACACTGTC 2653551

Qy 105 SerArgCysGlnGlyLysHisArg ----- 112

DB: 2653550 GACCGGCGCCAGGCAAGGGGAGGTGAGACCGGCAACAGGGTACCGTGATACCCTGGGACACTGTC 2653491

Qy 113 ----- ArgPheGluMetAspArgGluProLysSer----- 123

DB: 2653490 GTGGCCGATGGGGATGGGGAGGTGAGACCGTGGCAAGCTGGGATCGCTGTTGGGTAGAGTGGTGAATGTC 2653431

Qy 124 ArgTyrCysAlaGluCys----- 129

DB: 2653430 CGGCCGTGTCGCCACCTCGGGCTGGGTGGTATCCGGACCGTGCAGCAATGTC 2653371

Qy 130 ----- AsnArgLeuHisProAlaGlu----- 137

DB: 2653370 ATGGGGATGGGGATGGGGAGGTGAGACCGTGGCAAGCTGGGATCGCTGTTGGGTAGAGTGGTGAATGTC 2653311

Qy 137 ----- 137

DB: 2653310 GGCGACGGGATGGCAGATTGGCTGGCTGGGTGGTATCCGGACCGTGCAGCAATGTC 2653251

Qy 138 --- GlyAspPhePhePhePheAlaGlu----- 143

DB: 2653250 GCGGGGACCTCTACGTTGAGGCCCCATGGCTGGGCTGGGGAGGT 2653191

Qy 144 ----- SerSerMetLeuGlyLeuLysIsole 151

DB: 2653190 GACCATCTGGATTGACAGGGTTGGTGGCCATGGTGGGCTGGGTACGGTC 2653131

Qy 152 ThriYrPheAlaLeuMetAspGlyLysValTyraAspIleThrGlutTrpAlaGlycGln 171

GenCore version 5.1.6  
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### OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 1, 2003, 10:10:04 : Search time 362 Seconds

(without alignments)

2448.264 Million cell updates/sec

Title: US-10-049-742-11

Perfect score: 1433

Sequence: MAQVPEDELNPFLVIGEAT.....VPKGEAKPDKRKXVRPFQQR 269

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters:

4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Mininum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Command line parameters:

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-MDOB=frame+P2n.model -DEV=x1h
-Q=cgn2_1/USPETO.spool/US10049742/runat_01122003_073138_18649/app_query.fasta_1.455
-DB=PublishedApplications.NA.QFMT-fstab -SUFFIXx-rnpD -MINNATCH=blosum62
-LOCPIXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANSL=human40_cdi -LIST=-5 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 ALIGN=15 MODE=LOCAL -OUTFILE=pco -NORN=exc -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USERID=US10049742 @CGN 1 350 @runat 01122003_073138_18649
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=20 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -FGAPEXT=7 -YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6
-FGAPEXT=7 -YGAPEXT=7 -FGAPEXT=7 -YGAPEXT=7 -XGAPEXT=0.5 -DELOP=6
```

Database :

```
1: /cgn2_6/picodata/1/pubpna/0US07 PUBCOMB.seq:*
2: /cgn2_6/picodata/1/pubpna/PCT NEW PUB seq:*
3: /cgn2_6/picodata/1/pubpna/0US06 NEW PUB.seq:*
4: /cgn2_6/picodata/1/pubpna/0US06 PUBCOMB.seq:*
5: /cgn2_6/picodata/1/pubpna/0US07 NEW PUB.seq:*
6: /cgn2_6/picodata/1/pubpna/0CTUS PUBCOMB.seq:*
7: /cgn2_6/picodata/1/pubpna/0US08 NEW PUB.seq:*
8: /cgn2_6/picodata/1/pubpna/0US09 PUBCOMB.seq:*
9: /cgn2_6/picodata/1/pubpna/0US09A PUBCOMB.seq:*
10: /cgn2_6/picodata/1/pubpna/0US095 PUBCOMB.seq:*
11: /cgn2_6/picodata/1/pubpna/0US0C PUBCOMB.seq:*
12: /cgn2_6/picodata/1/pubpna/0US09 NEW PUB.seq:*
13: /cgn2_6/picodata/1/pubpna/0US10A PUBCOMB.seq:*
14: /cgn2_6/picodata/1/pubpna/0US10B PUBCOMB.seq:*
15: /cgn2_6/picodata/1/pubpna/0US10 NEW PUB.seq:*
16: /cgn2_6/picodata/1/pubpna/0US60 NEW PUB.seq:*
17: /cgn2_6/picodata/1/pubpna/0US60 PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### ALIGNMENTS

RESULT 1

US-10-198-846-12415/c

; Sequence 12415, Application US/10198846

; Publication No. US20030099974A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Xu, Yongyao

; APPLICANT: Wang, Youthen

; STEINMANN, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; THERAPY OF BREAST CANCER

; FILE REFERENCE: MRI-049

; CURRENT APPLICATION NUMBER: US/10/198,846

; CURRENT FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/306,220

; NUMBER OF SEQ ID NOS: 14084

; SEQ ID NO: 12415

; LENGTH: 2945

; TYPE: DNA

; ORGANISM: Homo sapiens

### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
C 1	1433	100.0	2945	US-10-198-846-12415 Sequence 12415, A

Alignment Scores:

Pred. No.:	Length:	2.71e-147
Score:	Matches:	2945
Percent Similarity:	Conservative:	1433.00
Best Local Similarity:	Mismatches:	100.00%
Query Match:	Indels:	100.00%
Db:	Gaps:	14

US-10-049-742-11 (1-269) × US-10-198-846-12415 (1-2945)

Qy 1 MetAlaGlyValProGluAspGluLeuAsnProPheHisValLeuGlyAlaGluAlaThr 20  
Db 1576 ATGGCTGGTGTCTGGATGAGCTAACCCCTTCATGTACTGGGGTAGGCCACA 1517

Qy 21 AlaSerAspValPheLeuLysLysAlaTyrArgGlnLeuAlaLavalMetValIleProAsp 40  
Db 1516 GCATCAGTTGAACTGAAGGCCTATAAGCTGGCATAGCTGGATGTTCATCTGAC 1457

Qy 41 LysAsnHisIleProAspGluAlaGluGluAlaPheLeuValLeuArgAlaAlaLysAspIle 60  
Db 1456 AAAATCATCATCCCCGGTGGAGCTGGCACATT 1397

Qy 61 ValSerAlaAlaGluLysArgLysGluLysGluLysGluMetAlaGluLysGluLeu 80  
Db 1396 GTCAGCATGGTCAAGGGAGGAGTATGATGAACTGGAGAGATGAGCT 1337

Qy 81 SerArgSerValAsnGluPheLeuSerLysIleGluLysAspAspLeuLysGluAlaMetAsn 100  
Db 1336 ACCGGTCACTGAAATGATGTTCTGTCRAAGCTCAAGGAGCAATGAAT 1277

Qy 101 ThrMetMetCysSerArgCysGlnGlyLysIleArgArgPheGluMetAspArgGluPro 120  
Db 1276 ACTATGATGTGATGCCATGGAAAGCATAGGGGTTGAAATGGACCGGGAACT 1217

Qy 121 LysSerAlaLysTyrCysAlaGluCysAsnArgLeuLysPheAlaGluGluLysAspPhe 140  
Db 1216 AAGAGTCCAGTACATGCTGTAATAGCTGATCTGCTGAGGAAGGACTT 1157

Qy 141 TrpAlaGluUserSerMetLeuGlyLysIleThrTyrPheAlaLeuMetAspGlyLys 160  
Db 1156 TGGCAGAAGTCAGCATGTTGSCCTCAAGATCACCTTGACATGATGGAAAG 1097

Qy 161 ValTy AspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHis 180  
Db 1096 GTGTATGACATCACAGGTGGCTGGATGCCATCTGAGTCAGCTGGATCTGGAC 1037

Qy 181 ArgValProTyrHistidineSerPheGlySerArgIleProGlyThrArgGlyArgGinArg 200  
Db 1036 AGAGTCCCTATCACATCTCATTTGGTCGATTCAGGACCAGGAGAGA 977

Qy 201 AlaThrProAspAlaProProAlaAspLeuUserArgIlePheGlnVal 220  
Db 976 GGCACCCAGATGCCCTCTGATCTGAGTTCTGAGTCAGCTGGATCTGGAC 917

Qy 221 ProProGlyGlnMetProAspGlyAsnAspPhePheAlaAlaLysProGlyIle 240  
Db 916 CCCCCAGGGCAGATGCCATCTGGAAACTTCCTGGAGCTGGCTGCCCTGGGCC 857

Qy 241 AlaAlaLysSerLysProAsnSerThrValIleProLysGlyGluAlaLysProLysArg 260  
Db 856 GTCGACCCCTPAGCCACAGCACGACAGCAAGGAGCAACCTAACGGCGGG 797

Qy 261 LysLysValArgArgProPheGlnArg 269  
Db 796 AAGAAACTGAGSAGGCCCTCCAACGT 770

RESULT 2  
US-09-814-353-19835/C  
Sequence 19835, Application US/09814353  
Publication No. US2003016581A1  
GENERAL INFORMATION:  
; APPLICANT: Lee, John  
; APPLICANT: Thompson, Pamela

Qy ; APPLICANT: Lillie, James  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER  
; FILE REFERENCE: MRL-0063  
; CURRENT APPLICATION NUMBER: US/09/814,353  
; CURRENT FILING DATE: 2001-03-21  
; PRIORITY APPLICATION NUMBER: US 60/191,031  
; PRIORITY FILING DATE: 2000-03-21  
; PRIORITY APPLICATION NUMBER: US 60/207,124  
; PRIORITY FILING DATE: 2000-05-25  
; PRIORITY APPLICATION NUMBER: US 60/211,940  
; PRIORITY FILING DATE: 2000-06-15  
; PRIORITY APPLICATION NUMBER: US 60/216,820  
; PRIORITY FILING DATE: 2000-07-07  
; PRIORITY APPLICATION NUMBER: US 60/220,661  
; PRIORITY FILING DATE: 2000-07-25  
; PRIORITY APPLICATION NUMBER: US 60/257,672  
; PRIORITY FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 22037  
; SOFTWARE: FastSeqQ For Windows Version 4.0  
SEQ ID NO: 19835  
LENGTH: 3090  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 488,-525  
OTHER INFORMATION: n = A,T,C or G

US-09-814-353-19835

Aligned Scores:

Pred. No.:	Length:	2.88e-147
Score:	Matches:	1433.00
Percent Similarity:	Conservative:	100.00%
Best Local Similarity:	Mismatches:	100.00%
Query Match:	Indels:	100.00%
DB:	Gaps:	12

US-10-049-742-11 (1-269) × US-09-814-353-19835 (1-3090)

Qy 1 MetAlaGlyValProGluAspGluLeuAsnProPheIleValProGlyIleValAlaThr 20  
Db 1570 ATGGCTGGGTRCTGGATGAGCTAACCTTTCATGACTGGGGTIGAGGCCACA 1511

Qy 21 AlaSerAspValGluLeuLysSalaIleTyrArgGlnLeuIaLvaMetVaHisProAsp 40  
Db 1510 GATCAAATGTTGAACTGGCTTAAAGGGCTATAAACGTTGAGTTATCCGAC 1451

Qy 41 LysAsnHisIleProGluGalaGluGluAlaPheLysValLeuArgIaaAlaIlePhe 60  
Db 1450 AAAAATCATCATCCCCGGCTGAGGACGCCCTCAAGGTTTGGAGCTGGACATT 1391

Qy 61 ValSerAlaLysArgLysGlyGluLysTyrGluMetLysArgMetAlaGluLysGluLeu 80  
Db 1390 GTCAAGGAAATGCTGAAAGCAAGGAAAGGTATGAGATGAAACGATGAGATGAGCTG 1331

Qy 81 SerArgSerValAsnGluPheLeuSerLysLeuGlyAspAspLysLeuLysGluAlaMetAsn 100  
Db 1330 AGCCGGTCAGTAAATGTTGCAAGATGCTGAGCTGGAGGAACTGAAT 1271

Qy 101 ThrMetMetCysSerArgCysGlnGlyLysIleThrTyrPheAlaLeuMetAspArgGluPro 120  
Db 1270 ACTATGATGTGCTAGCCGATGCCAGTGGATTTGAAATGGACGGGAACT 1211

Qy 121 LysSerAlaArgGlyArgSerAlaGluCysAsnArgLeuSerGluLysLeuGlyAspPhe 140  
Db 1210 AAAGGGCCAGATACTGTGCTGAGTGTAAATAGGCTCATCTGCTAGGAGGAGCTT 1151

Qy 141 TrpAlaGluSerSerMetLeuGlyIleLysIleThrTyrPheAlaLeuMetAspGlyLys 160  
Db 1150 TGGCCAGAGTCAGCTAACGCTCAAGTGGCTCAAGATGCTGACTTGCACTGATGGAAAG 1091

Qy	161	ValTyrAspIleThrGluIrrAlaAlaGlyLysGlnArgValGlyIleSerProAspThrHis	180	Qy	149	LeuIysIleThrTyrPheAlaLeuMetAspGlyLysValTyrAspIleIthrGluIrrAla	168		
Db	1090	GRCATGAGTCAGCTGGGTGGATCCACCGTGTAGATCTCCAGATAACCAC	1031	Db	242	CTCAAGATCACCCTACTTGCACTGATGGTGAAGGTATGATCAGAGGGCT 301			
Qy	181	ArgValProTyrHisIleSerPheGlySerArgIleProGlyThrArgIleArgGlnArg	200	Qy	169	GlycysGlnArgValGlyIleSerProAspThrHisArgValProTyrHisIleSerPhe	188		
Db	1030	AGATGCCCTATCACATCCTCATGTTGTCGATTCAAGGACCAAGGGCAGAGA	971	Db	302	GGATGCCAACGGTGAATCTCCAGATAACCAAGATCCTATCACATCCTATT 361			
Qy	201	AlaIthrProAspAlaProProAlaAspPheLeuSerArgIlePheGlnVal 220		Qy	189	GlySerArgIleProGlyThrArgIleArgGlnArgAlaIthrProAspAlaProProAla	208		
Db	970	GCCACCCCGAGATGCCCTCTGCTGATCTTCAGATTCTTCAGATTCAGTA	911	Db	362	GGTTCCTGGATTCAGGACCAAGGGACCCAGAGAGCCACGGCAGATGCCCTCTCTGCT 421			
Qy	221	ProProGlyGlnMetProAsnGlyAsnPheHeAlaIlaProGlnProGlyAla	240	Qy	209	AspIleGlnAspPheLeuSerArgIlePheGlnValProProGlyGlnNetProAsnGly	228		
Db	910	CCCCAGGGAGATGCCATGGAACTTGTGAGTCTCAGCTGCCCCTGGAGC	851	Db	422	GATTTCTCAGGATTCCTGAGTCGATCTTCAGATGCCAGATGCCAAAT-GGG	480		
Qy	241	AlaAlaAlaSerIlysProAsnSerThrValIlysGlyGluAlaLysProlysArgArg	260	Qy	229	AsnPhePheAlaAlaAlaProGlnProAlaProGlyAlaAlaAlaSerIlysProlysSer	248		
Db	850	GCTGCAGSCTCPAAGCCCAACAGACAGTACCCAGGAAACCTAACCTAACCTAAGGGGG	791	Db	481	AACTCTTTCAGCTCCAGCCTGAGCTTCAGCTGCCCTGGAGCGAGCTCAAGGCCAACAGC	540		
Qy	261	LysLysValArgArgPropheGlnArg	269	Qy	249	ThrValIlysProlysGlyGluAlaLysProlysArgArgLysValArgArgPropheGin	268		
Db	790	AAAAGAAACTGAGGGGGCCCTCCAGCT 764		Db	541	ACAGTACCCAAAGGAGAAGCCAAACTAACCTAACGCGGAAAGTGAAGGGCCCTCCAA	600		
<hr/>									
RESULT 3									
US-10-096-534-43		; Sequence 43 , Application US/10096534		Qy	269	Arg	269		
		; Publication No. US20030166887A1		Db	601	CGT	603		
		; GENERAL INFORMATION:		<hr/>					
		; APPLICANT: The Brigham and Women's Hospital, Inc.		RESULT 4					
		; APPLICANT: Miuno, Shuichi		US-10-097-340-182					
		; APPLICANT: Glowacki, Julie		Publication No. US20030087250A1					
		; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS		GENERAL INFORMATION:					
		; FILE REFERENCE: B0801/172/KA/ERP		APPLICANT: John MONAHAN					
		; CURRENT FILING DATE: 2002-03-12		APPLICANT: Manjula GANNAVARAM					
		; PRIOR APPLICATION NUMBER: US 60/274, 980		APPLICANT: Sebastian HOERSCH					
		; PRIOR FILING DATE: 2001-03-12		APPLICANT: Shubhangi KAMATKAR					
		; NUMBER OF SEQ ID NOS: 79		APPLICANT: Steve G. KOVATS					
		; SOFTWARE: Patentin version 3.0		APPLICANT: Rachel E. MEYERS					
		; SEQ ID NO: 43		APPLICANT: Michael MORRISEY					
		; LENGTH: 754		APPLICANT: Peter OLANDT					
		; TYPE: DNA		APPLICANT: Aimi SEN					
		; ORGANISM: Homo sapiens		APPLICANT: Peter VEIBY					
US-10-096-534-43				APPLICANT: Gordon B. MILLS					
				APPLICANT: Robert C. BAST, Jr.					
				APPLICANT: Karen LU					
				APPLICANT: Rosemarie SCHMANDT					
				APPLICANT: Xumei ZHAO					
				PRIOR APPLICATION NUMBER: Karen GLATT					
				TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,					
				TITLE OF INVENTION: Assessment, Prevention, and Therapy Of Ovarian Cancer					
				FILE REFERENCE: MRI-030					
				CURRENT APPLICATION NUMBER: US/10/097, 340					
				CURRENT FILING DATE: 2002-03-14					
				PRIOR APPLICATION NUMBER: 60/276, 025					
				PRIOR FILING DATE: 2001-03-14					
				PRIOR APPLICATION NUMBER: 60/325, 149					
				PRIOR FILING DATE: 2001-09-26					
				PRIOR APPLICATION NUMBER: 60/276, 026					
				PRIOR APPLICATION NUMBER: 60/324, 967					
				PRIOR FILING DATE: 2001/09/26					
				PRIOR APPLICATION NUMBER: 60/311, 732					
				PRIOR FILING DATE: 2001-08-10					
				PRIOR APPLICATION NUMBER: 60/325, 102					
				PRIOR FILING DATE: 2001-09-26					
				PRIOR APPLICATION NUMBER: 60/323, 580					
				NUMBER OF SEQ ID NOS: 363					
				SOFTWARE: FastSEQ for Windows Version 4.0					
				SEQ ID NO: 182					
				LENGTH: 754					
				TYPE: DNA					

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ORGANISM: Homo sapiens  
US-10-097-340-182

Alignment Scores:  
Pred. No.: 4.38e-106 Length: 754  
Score: 1051.00 Matches: 200  
Percent Similarity: 99.50% Conservative: 0  
Best Local Similarity: 99.50% Mismatches: 0  
Query Match: 73.34% Indels: 1  
DB: 14 Gaps: 0

US-10-049-742-11 (1-269) × US-10-097-340-182 (1-754)

QY 69 GlutYrGluMetLysArgMetAlaGluAsnGluIleSerArgSerValAsnGluPheLeu 88  
DB 2 GAGTAGATGAAACGATAAGTGGCAAGATGAGCTGAGCTGAGGTACTGACTTCG 61

QY 89 SerLysLegLysIlePaspIleLysGluAlaMetAsnThrMetMetCYSerArgCysGln 108  
DB 62 TCCAAAGCTGCAAGATGACCTCAAGGGAATGATACTATGATGTTGAGCCATGCCA 121

QY 109 GlyLysHisArgArgPheGluIleMetAspArgPheGluProLysSerAlaArgYrCysAlaGlu 128  
DB 122 GGAAAGCATAGGAGTTGAAATGACCGGAACCTAACAGTGCAGATACTGTCGAG 181

QY 129 CysAsnArgLeuHisProAlaGluGluGlyAspPheTrpAlaGluUserSerMetLeuGly 148  
DB 182 TGATATAGGCTGCATCCCTCTGAGAAAGGAGACTTTGGCCAGAGTCAGGCATGGCC 241

QY 149 LeuLysIleThrTyrPhaAlaLeuMetAspGlyLysValTyrAspIleThrGluTrpAla 168  
DB 242 CTCAAGATACCTACTTCACTGATGGTAAAGGTTGATGACATCPACAGTGTTGGGT 301

QY 169 GlycYsGlnArgValGlyIleSerProAspThrHisArgValProTyRHisIleSerPhe 188  
DB 302 GGATGCCACGGTAGGTATCTCCCAGTACCAAGATCCCTATCACATCTATT 361

QY 189 GlySerArgIleProGlyThraGlyArgGlnArgAlaThrProAspAlaProProAla 208  
DB 362 GGTTCTCGGATTCCAGGCCACGGCCAGCAGGGCCAGAGGCCACCCAGATCCCTCTGGT 421

QY 209 AspIleGlnAspPheLeuSerArgIlePheGlnValProProGlyGlnMetProAsnGly 228  
DB 422 GATCTTCAGATTCTTGATCTTGCAACTTCAAGTACCCCGAGGCAAT-GGG 480

QY 229 AsnPhePheAlaAlaAlaProGlyAlaAlaAlaSerLysProAsnSer 248  
DB 481 AACCTCTTGCAGETCCPAGCCCTGGACCCGCTGAGGCCAACCGC 540

QY 249 ThralValPheLysGlyGluLalaLysProlysArgArgLysLysValArgProPheGln 268  
DB 541 ACAGTACCCAAAGGGAGAACCTAACGGGAAAGCTAACGGGCCAACCTAAC 600

QY 269 Arg 269  
DB 601 CGT 603

RESULT 5  
US-09-764-891-8949  
Sequence 8949, Application US/09764891  
Publication No. US20030077808A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: P006  
CURRENT APPLICATION NUMBER: US/09/764,891  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10231  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 8949  
LENGTH: 7453  
TYPE: DNA

;

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (350)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-891-8949

Alignment Scores:  
Pred. No.: 1.46e-100 Length: 7453  
Score: 1012.50 Matches: 231  
Percent Similarity: 45.21% Conservative: 0  
Best Local Similarity: 45.21% Mismatches: 0  
Query Match: 70.66% Indels: 280  
DB: 11 Gaps: 4

US-10-049-742-11 (1-269) × US-09-764-891-8949 (1-7453)

QY 37 ValHisProAspLysAsnLysIleHisProArgAlaPheLysValLeuArgAla 56  
DB 1996 GTTCATCTGACAAAATCATCATCCCGCGCTAGGAGGCCCTAACGGTTGGAGCA 2055

QY 57 AlaArgPaspIleValSerAsnAlaGluLysArgLysGluTyrglumet-----72  
DB 2056 GCTTGGACATTGTGAGCATGTCGAAAGGAAAGGATGAGCATGTCATGGAGCA 2114

QY 72 -----72

DB 2115 TGGAAATCATCAGATAATGTAATGAAATCTCAAATAGCAAGGGCATCTGACTTG 2174

QY 72 -----72

DB 2175 GGGTGGAGGCTTGTGAGATGGAGAACTGAGTCACITGCTCTCTGCTAGACAGG 2234

QY 72 -----72

DB 2235 GGCCCTCAAGAGGCCAACTGATATGTCCTCTCCCTGATAATCCTTCGTCGACTTA 2294

QY 73 -----LybArgMetAlaGluAsnGlutieuserArgSerValAsn 85  
DB 2295 CAAAGCATTCTTCCTATTAGGAAGAACGAAATGGCAAGAACGCGGTCACTAAAT 2354

QY 86 GluPheLeuSerIleGlnAspAspIleLysGluAlaMetAsnThrMetMyCysSer 105  
DB 2355 GAGTTCTCTCCAGCTGAAAGTGAACCTCAAGGCAATGACATGAACTATGATGTAGC 2414

QY 106 ArgCysGlnGlyLysHis-----111

DB 2415 CGATGCCAAGGAAAGCATAGGTATGAAATAGAAGGAGGGATGGACATCAAGCTCA 2474

QY 111 -----111

DB 2475 GGGATATGTAACCAAGGATCTTAGTGAATGACTGGTAATTATGAGTTACATCTGTAT 2534

QY 111 -----111

DB 2535 CTGATATAATTAGTAAAAAGACCCCTTAAGTTCTACCTTGTCAATATGTCATATGACTGAC 2594

QY 111 -----111

DB 2595 GATTTAAATTAGCAGTAAAGAACATAGCTTAAAGGATATGAAAT 2654

QY 111 -----111

DB 2655 ACTAAATGGGGTAATTTPAGATGTTCAAGCCCTATTGTAATGGTAAGACTACTAG 2714

QY 112 -----112

DB 2715 CAGTGGCCCTAGGTAGGCTTGACAATTTAAAGGAACATATCCTTGTGTTGAGGGAG 2774

QY 113 gPheGluMetAspArgGluProLysSerAlaArgTyrcysAlaGluCysAsnArgLeuH1 133  
DB 2775 GTTGAAATGGACGGGACCTAACGGTCAAGATCTGCTGAGTGTGAACTGTGCTGCA 2834



WS-10-049-742-11 {1-269} x WS-10-228-405A-10 [1-12572]

卷之三

8-1 Application US/10134288  
in No. US20030165520A1  
FORMATION:  
: Cao, Xumei  
: Sheppard, Mike  
INVENTION: ATTENUATED FORMS OF BOVINE VIRAL DIARRHEA VIRUS  
APPLICATION NUMBER: US/10/134,288  
FILING DATE: 2002-04-29  
APPLICATION NUMBER: US/09/702,330  
FILING DATE: 2000-10-31  
APPLICATION NUMBER: 09/433,262  
FILING DATE: 1999-11-04  
SEQ ID NOS: 9  
Patent In Ver. 2.0  
1 14078  
A : Bovine Viral Diarrhea Virus

cores:	1.47e-43	Length:	14078
clarity:	497.00	Matches:	89
similarity:	98.90%	Conservative:	1
	97.80%	Mismatches:	1
	34.68%	Indels:	0
	12	Gaps:	0

2-11 (1-269) x US-10-134-288-1 {1-14078}	3 MetCysSerArgCysGlnGlyLysHiSArgArgPheGluMetAspArgPheGluProLySer 122
	2 ATGTCAGCCATGCCAGGAAGCATAGGAGTTAAATGGACCGGAACTTAAGGT 4591
	3 AlaArgTyrCysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspPheTerPheAla 142
	2 GCGAGGACTGTGCTGAGTGTAAATTGGCTGCATCTGTGAGGAAGGAGCTTTGGCA 4651
	3 GluSerSerMetLeuGlyLeuLysIleThrTyrPheAlaLeuMetAspGlyLysValTyr 162
	2 GAGTCCAGCAATTGGCCCTCAAATACCTACTTGGCTGATGGATGAAAGGTGTAT 4711
	3 AspIleThrGluTrpAlaGlyCysGlnArgValGlyIleSerProAspThrHisArgVal 182
	2 GATATAACAGGTGGTGGAAAGCCASGTCAGTCCCAGATACCCACAGAGTC 4771
	3 ProTyRHisIleSerPheGlySerArgIlePro 193

OTHER INFORMATION: pNADL890 vector

US-10-228-406A-9

Alignment Scores:	
Pred. No.:	1. 84e-43
Score:	497.00
Percent Similarity:	98.90%
Best Local Similarity:	97.80%
Query Match:	34.68%
DB:	14
	0

US-10-049-742-11 (1-269) x US-10-228-406A-9 (1-16713)

Qy	Length: 16713
Db	Length: 89
103 Met Cys Ser Arg Cys Glu Gly Leu Ile His Arg Val Gln Asp Glu Met Asp Arg Glu Pro Lys Ser Pro Asp Ala Glu Glu Gly Asp Pro Asp Thr Ala 1-22	Conservative: 1
4988 ATGTGCA GCG GTGCC CGGG AAAGC ATGG AGTT GAAAT GGAC CCG GAA CCT AAG AGT 5047	Mismatches: 1
123 Ala Arg Gty Tyr Cys Alan Glu Cys Alan Arg Leu His Pro Pro Ala Glu Glu Gly Leu Ile His Arg Val Gln Asp Glu Met Asp Arg Glu Pro Lys Ser Pro Asp Ala Glu Glu Gly Asp Pro Asp Thr Ala 1-42	Indels: 0
5048 GCC AGA TACT GTG CTG GTG TAAT AGGT GCAT CCT GCT GAG GTG ACT TT CGG CA 5107	Gaps: 0
143 Glu Ser Ser Met Leu Gly Leu Ile Thr Tyr Phe Ala Leu Met Asp Gly Lys Val Tyr 1-62	
5108 GAG TCG AGC ATG TGG CCT CAA AAC GCT ACT TT GGC CCT GAG GTG AAAG GTG TAT 5167	
163 Asp Ile Thr Glu Thr Ala Gly Cys Glu DArg Val Gly Ile Ser Pro Asp Thr His Arg Val 1-82	
5168 GAT AT CAG AGT GGG CTG GG AT CCA GGG TA CCT CCC AGA AT ACC CAC AGTC 5227	
183 Pro Tyro His Ile Ser Gly Ser Arg Ile Pro 1-93	
5228 CCT TG CAC ACAT TCAT TT GGT AC GG AT GC CT 5260	

RESULT 10

US-09-814-353-1424/C<sub>c</sub>

Sequence 1424, Application US/09B14353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF OVARIAN CANCER

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US/09/814,353

PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SEQ ID NO 1424  
LENGTH: 259  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1, 2  
OTHER INFORMATION: n = A,T,C or G

SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1424  
LENGTH: 259  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1, 2  
OTHER INFORMATION: n = A,T,C or G

Alignment Scores:  
Pred. No.: 2.58e-40 Length: 259  
Score: 447.00 Matches: 85  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 31.19% Indels: 0  
DB: 12 Gaps: 0

US-10-049-742-11 (1-269) x US-09-814-353-7786 (1-259)

Qy 30 TyrArgGlnLeuAlaValMetValHisProAspLysAsnHisProArgAlaGluGlu 49  
Db 258 TATAGCACGGCTGGCAGTGATGTTGCAGCTGGACATTGGCAATGCTGAAATGCTGAGCTTCAGGTGTTGCAGCAGCTGGACATTGGTACGAAATGCTGAAAGGAAAGGAG 139

Qy 50 AlaPhelysValleuArgAlaAlaIrrAspIlevalSerAsnAlaGluLysArgLysGlu 69  
Db 198 GCCTTAAGGTTTGCAGCTGGCAATGCTGAAATGCTGAAAGGAAAGGAG 139

Qy 70 TyrGluMetLysArgMetAlaGluAsnGluLeuSerArgSerValLeuSer 89  
Db 138 TATGAGTAGAAGGAAATGGAATGGCAGATGGCAATGCTGCAATGCTGAAAGGAG 139

Qy 90 LysLeuGlnAspIleuLysGluAlaMetAsnThrMetCysSerArgCysGlnGly 109  
Db 138 TATGAGTAGAAGGAAATGGAATGGCAGATGGCAATGCTGCAATGCTGAAAGGAG 139

Qy 110 LysHisArgArgPhe 114  
Db 18 AAGCATAGGAGGTTT 4

RESULT 11  
US-09-814-353-7786/c  
Sequence 7786 Application US/09814353  
Publication No. US20030165831A1  
GENERAL INFORMATION:  
APPLICANT: Lee, John  
APPLICANT: Thompson, Pamela  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF OVARIAN CANCER  
FILE REFERENCE: MRI-006B  
CURRENT APPLICATION NUMBER: US/09/814/353  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: US 60/191,031  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SEQ ID NO 7786  
LENGTH: 259  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1, 2  
OTHER INFORMATION: n = A,T,C or G

Alignment Scores:  
Pred. No.: 2.58e-40 Length: 259  
Score: 447.00 Matches: 85  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 31.19% Indels: 0  
DB: 12 Gaps: 0

US-10-049-742-11 (1-269) x US-09-814-353-7786 (1-259)

Qy 30 TyrArgGlnLeuAlaValMetValHisProAspLysAsnHisProArgAlaGluGlu 49  
Db 258 TATAGAACGCTGGCAGCTGGACATTGGTACGAAATGCTGAAAGGAAAGGAG 139

Qy 50 AlaPhelysValleuArgAlaAlaIrrAspIlevalSerAsnAlaGluLysArgLysGlu 69  
Db 198 GCCTTAAGGTTTGCAGCTGGCAATGCTGAAATGCTGAAAGGAAAGGAG 139

Qy 70 TyrGluMetLysArgMetAlaGluAsnGluLeuSerArgSerValLeuSer 89  
Db 138 TATGAGTAGAAGGAAATGGAATGGCAGATGGCAATGCTGCAATGCTGAAAGGAG 139

Qy 90 LysLeuGlnAspIleuLysGluAlaMetAsnThrMetCysSerArgCysGlnGly 109  
Db 138 TATGAGTAGAAGGAAATGGAATGGCAGATGGCAATGCTGCAATGCTGAAAGGAG 139

Qy 110 LysHisArgArgPhe 114  
Db 18 AAGCATAGGAGGTTT 4

RESULT 12  
US-09-764-868-175  
Sequence 175 Application US/09764868  
Patent No. US2002016871A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: P1232  
CURRENT APPLICATION NUMBER: US/09/764,868  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION DATA REMOVED - REFER TO PALM OR FILE WRAPPER  
NUMBER OF SEQ ID NOS: 1510  
SEQ ID NO 175  
LENGTH: 1030  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (776)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (923)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (1002)  
OTHER INFORMATION: n equals a,t,g, or c

US-09-764-868-175



RESULT 15  
 US-10-198-846-5395  
 Sequence 5395, Application US/10198846  
 Publication No. US20030099974A1  
 GENERAL INFORMATION:  
 APPLICANT: Lillie, James  
 APPLICANT: Wang, Youyan  
 APPLICANT: Steimann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF BREAST CANCER  
 TITLE OF INVENTION: THERAPY OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198-846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 5395  
 LENGTH: 928  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 413, 430, 468, 500, 519, 521, 537, 546, 551, 559, 571,  
 LOCATION: 581, 586, 589, 592, 608, 615, 640, 644, 652, 653, 664, 676,  
 LOCATION: 679, 685, 690, 695, 699, 706, 707, 721, 722, 725, 730,  
 LOCATION: 740, 742, 754, 761, 765, 769, 775, 777, 794, 807, 813  
 OTHER INFORMATION: n = A,T,C or G  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 817, 819, 831, 833, 837, 840, 845, 851, 852, 858, 860, 861,  
 LOCATION: 864, 865, 867, 868, 877, 878, 879, 880, 881, 884, 886, 897,  
 LOCATION: 899, 900, 905, 912, 913, 918, 919, 920, 924, 927, 928  
 OTHER INFORMATION: n = A,T,C or G

US-10-198-846-5395

Alignment Scores:  
 Pred. No.: 2.95e-10 Length: 928  
 Score: 180.00 Matches: 38  
 Percent Similarity: 60.24% Conservative: 12  
 Best Local Similarity: 45.78% N mismatches: 33  
 Query Match: 12.56% Indels: 0  
 DB: 14 Gaps: 0

US-10-049-742-11 (1-269) x US-10-198-846-5395 (1-928)

Qy 3 GlyValProGluAspGluLeuAsnProPheHisValLeuGlyValGluAlaThrAlaSer 22  
 Qy 4 GlAGCTCACCCTGGGGCGCCGGCAAGTGAACTTCAGCAAACTGGT 65  
 Db 5 GATGAATTGAAAAAGCTTATGAAAGCTTGTGAAAGTTTCATCCAGCAAAAC 125

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

US-10-198-846-5395

Qy 12 PheHisValLeuGlyValGluAlaThrAlaSerAspValGluLeuLysAlaThrArg 31  
 Db 1416 TATGAGATCTGGGGTGAGGAAGGGCTGGATGAGAACCTGAGAACGCCAACCGC 475

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

Qy 32 GluLeuAlaValMetValHisProAlaLysProArgAlaGluGluAlaPhe 51  
 Db 476 AGACTGGCCCAAATCCACCGAACAGAACCCGCACTGGCCACTGAAAGCTTC 535

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

Qy 52 LysValLeuArgAlaAlaLysProLeuValSerAsnAlaGluLysGluLysGlu 71  
 Db 536 AAAGCCATTCGGCACGATGCGTACTAGCAACCGGAAAGGAAACGATGAC 595

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

Qy 72 MetLysArgMetAlaGluAsnGluLeuSerArgSerValAsnGluPheLeuSerLysLeu 91  
 Db 596 -----CAGTTC 601

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

Qy 92 GlnAspAspLeuLysGluAlaMetAsnThrMetCysSerArgCysGlnGlyLys-- 110  
 Db 602 GGCGATGACAGGAGCCAGGCCCCG-----CACGGCCATGGG 640

US-10-049-742-11 (1-269) x US-10-252-157-105 (1-3025)

Alignment Scores:  
 Pred. No.: 1.4e-10 Length: 3025  
 Score: 189.00 Matches: 44  
 Percent Similarity: 50.43% Conservative: 14  
 Best Local Similarity: 38.26% Mismatches: 27  
 Query Match: 13.19% Indels: 30  
 DB: 12 Gaps: 3

Qy 111 -----HisArgArgPheGluMetAspArgGluProLys 121  
 Db 641 CATGGGATTCACCGTGGCTTGGCCACATCCCTGAA 685

Search completed: December 1, 2003, 12:12:32  
 Job time : 396 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 1, 2003, 09:38:38 ; Search time 2530 Seconds  
(without alignments)  
2584.152 Million cell updates/sec

## SUMMARIES

	Result No.	Score	Query	Match	Length	DB ID	Description	
Title:	1	1361	95.0	2300	11	AK017830	Mus muscu	
Perfect score:	2	1361	95.0	2639	11	AK02681	Mus muscu	
Sequence:	3	1361	95.0	2712	11	AK05445	Mus muscu	
Scoring table:	4	1354	94.5	4231	11	AK02579	Mus muscu	
BLOSUM62	5	1348	94.1	3022	11	AK05345	Mus muscu	
Xgapop 10.0 , Xgapext 0.5	6	1337	93.3	4053	11	AK083878	Mus muscu	
Ygapop 10.0 , Ygapext 0.5	7	1280	89.3	942	13	BU538214	AGENCOURT	
Fgapop 6.0 , Fgapext 7.0	8	1240	86.5	955	13	BU58351	AGENCOURT	
Delop 6.0 , Delext 7.0	9	1224	85.4	957	12	BM802135	AGENCOURT	
Searched:	10	1189	83.0	918	13	BU95189	AGENCOURT	
22781392 seqs, 12152238056 residues	11	1138	79.4	878	12	BG73500	602735591	
Total number of hits satisfying chosen parameters:	12	1138	79.4	904	13	BO691177	AGENCOURT	
Minimum DB seq length: 0	13	1076.5	75.1	723	10	BE779250	60146514	
Maximum DB seq length: 2000000000	14	1076.5	75.1	927	12	BM42147	AGENCOURT	
Post-processing: Minimum Match 0%	15	1034	72.2	874	10	BF679562	602153994	
Maximum Match 100%	c	16	1025	71.5	737	14	CB324690	UI-R-D20
Listing first 45 summaries	c	17	1020	71.2	756	12	BGB63350	602787804
Maximum Match 100%	c	18	1018	71.0	871	10	BF139916	601789432
Listing first 45 summaries	c	19	1013	70.7	900	10	BG298053	602396271
Minimum DB seq length: 0	c	20	1005.5	70.2	787	13	BU288529	603608051
Maximum DB seq length: 2000000000	c	21	989	69.0	679	9	AW146163	urn:38bb12.x
Post-processing: Minimum Match 0%	c	22	973	67.9	785	12	BI333110	602993387
Maximum Match 100%	c	23	969	67.6	670	13	BUT08368	UI-M-FC0-
Listing first 45 summaries	c	24	964	67.3	667	14	BY762668	UY760298
Minimum DB seq length: 0	c	25	964.5	66.1	675	13	BGB63350	602787804
Maximum Match 100%	c	26	940	65.6	723	10	BE619407	601473229
Listing first 45 summaries	c	27	930	64.9	560	9	AV602887	AV602887
Minimum DB seq length: 0	c	28	927	64.7	715	13	BUT323784	603493402
Maximum Match 100%	c	29	919	64.1	676	13	BUC229462	603405604
Listing first 45 summaries	c	30	887	61.9	651	10	BB465186	BB465186
Minimum DB seq length: 0	c	31	864	60.3	645	13	BU371701	603811742
Maximum Match 100%	c	32	854	59.6	781	14	CB520550	UI-M-G10-
Listing first 45 summaries	c	33	837	58.4	912	10	BG751088	602728789
Minimum DB seq length: 0	c	34	835	58.3	810	13	BU247142	603551604
Maximum Match 100%	c	35	821	57.3	598	12	BU219192	603108110
Listing first 45 summaries	c	36	812	56.7	810	13	BU219192	603108110
Minimum DB seq length: 0	c	37	809.5	56.5	527	12	BI002288	BM1-HN007
Maximum Match 100%	c	38	796	55.5	618	12	BM011379	603635574
Listing first 45 summaries	c	39	796	55.5	857	13	BU900250	AGENCOURT
Minimum DB seq length: 0	c	40	794	55.4	481	10	BF722658	mab34906.
Maximum Match 100%	c	41	794	55.4	605	11	BX090711	EX090711
Listing first 45 summaries	c	42	793	55.3	467	10	BE864884	UI-M-BH1-
Minimum DB seq length: 0	c	43	786	54.8	448	12	BI002295	BM1-HN007
Maximum Match 100%	c	44	785	54.8	683	13	BG287112	604166695
Listing first 45 summaries	c	45	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	46	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	47	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	48	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	49	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	50	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	51	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	52	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	53	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	54	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	55	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	56	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	57	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	58	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	59	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	60	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	61	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	62	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	63	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	64	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	65	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	66	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	67	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	68	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	69	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	70	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	71	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	72	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	73	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	74	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	75	783	54.6	453	9	AI504202	vK90d12.x
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Maximum Match 100%	c	77	783	54.6	453	9	AI504202	vK90d12.x
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Minimum DB seq length: 0	c	79	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	80	783	54.6	453	9	AI504202	vK90d12.x
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Maximum Match 100%	c	83	783	54.6	453	9	AI504202	vK90d12.x
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Minimum DB seq length: 0	c	85	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	86	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	87	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	88	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	89	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	90	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	91	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	92	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	93	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	94	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	95	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	96	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	97	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	98	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	99	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	100	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	101	783	54.6	453	9	AI504202	vK90d12.x
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Minimum DB seq length: 0	c	103	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	104	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	105	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	106	783	54.6	453	9	AI504202	vK90d12.x
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Minimum DB seq length: 0	c	109	783	54.6	453	9	AI504202	vK90d12.x
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Minimum DB seq length: 0	c	118	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	119	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	120	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	121	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	122	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	123	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	124	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	125	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	126	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	127	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	128	783	54.6	453	9	AI504202	vK90d12.x
Listing first 45 summaries	c	129	783	54.6	453	9	AI504202	vK90d12.x
Minimum DB seq length: 0	c	130	783	54.6	453	9	AI504202	vK90d12.x
Maximum Match 100%	c	131	783	54.6	453	9		



Qy	21	AlaSerAspValGluLeuLysLysAlaTyrArgGlnLeuAlaValMetValHisProAsp	40		REFERENCE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Carninci,P., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Db	1459	GCATCGACATGAACTAAAGGCTATAAGCACTAGGAACTGGCATATGGCCATCTGAT	1518		AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Qy	41	LYSASHIHSisProArgAlaGluGluValAlaPheLysValLeuArgAlaAlaTrpAspIle	60		TITLE	Genome Res. 10 (10), 1617-1630 (2000)
Db	1519	AAAAAATCACCATCCCCGGCTGAGGGCCTCAAATTGGGCCAGCTGGCACATT	1578		JOURNAL	
Qy	61	ValSerAsnAlaGluLysAlaLysGluturyGluLysLysArgMetAlaGluAsnGluLeu	80		MEDLINE	2049374
Db	1579	GTCAGAACCCAGAGGGGGAGGATATGAGATGAACGATGGCAGAGATGGCTC	1638		PUBMED	11042159
Qy	81	SerArgSerValAlaGluPheLeuSerLysLeuGlnAspAspLeuLysGluAlaMetAsn	100		REFERENCE	Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Iishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsushita,H., Sakaguchi,S., Ikegami,T., Kashiwabiki,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
Db	1639	AGCCGGTCAGTGAAACTACAGATGACTCAAGGCAATGAACTGATGAACTGAA	1698		AUTHORS	RIKEN integrated sequence analysis (RSA) system -384 format sequencing pipeline with 384 multiplex sequencer
Qy	101	ThrMetMetCysSerArgCYSGLINGLYLysLysArgLysArgPheGluMetAspArgLypIle	120		TITLE	Genome Res. 10 (11), 1757-1771 (2000)
Db	1699	ACGATGATGTCAGCGATGCCAGGATGCCAGGAAAGGATAGGAGCTTGAAATGGACGGGAAACC	1758		JOURNAL	
Qy	121	LysSerAlaArgTyrCysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspPhe	140		MEDLINE	20530913
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Qy	141	TrpAlaGluUserSerMetLeuGlyLeuLysTleThr-TyrPheAlaLeuMetAspGlyLys	160		REFERENCE	Kawai,J., Shinagawa,A., Shidata,K., Yoshino,M., Itoh,M., Itoh,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamamoto,I., Saico,T., Okazaki,Y., Gojobori,T., Boni,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nakabu,I., Pesole,G., Quackenbush,J., Schriml,L.M., Stabukidze,F., Suzuki,R., Tomita,M., Wagner,J., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bult,C., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamia,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,J., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shiba,Y., Storch,K.P., Suzuki,H., Toyo-Oka,K., Wang,K.H., Weitz,C., Whitaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohetsuki,S., and Hayashizaki,Y.
Db	1819	TGGCAGAGCTGAGCTGAGCATGCTGGCCCTCAAGATCACTACTTGCCTGATGCAAGAAC	1878		AUTHORS	Functional annotation of a full-length mouse cDNA collection
Qy	161	ValTyrAspIleThrGluTrpAlaGlyCYSglnArgValGlyIleSerPirAspThrHis	180		TITLE	Nature 409 (6821), 685-690 (2001)
Db	1879	GTTGATGACTCACAGAGTGGCTGATGGCTGATGCCGCTGGTATCTCCCGATACTCAC	1938		JOURNAL	
Qy	181	ArgValProCysThrIleSerPheGlySerArgIleProGlyThrArgGlyArgGlnArg	200		MEDLINE	
Db	1939	AGAGTCCTAACATCATGGTCTGGTCACTGGGACACAGTGCCGCAAGGCAAGG	1998		PUBMED	11217851
Qy	201	AlaThrProAspAlaProProAlaAspLeuGlnAspPheLeuSerArgIlePheGlnVal	220		REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1999	GCCACTCCAGTCCCTCTGCTGACCTTGAGGATTCTTGACCGGGATTTCAAGTA	2058		TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Qy	221	ProProGlyGinMetProAsnGlyAsnPhenpheAlaAlaProGlnProAlaProGlyAla	240		JOURNAL	Nature 420, 563-575 (2002)
Db	2059	CCTCCGGCCGATGTCACAATGGAACTTCTGGCAACTCACCTGGCTGGACCC	2118		MEDLINE	
Qy	241	AlaAlaAlaSerLysProAsnSerThrValProLeuGlyGluAlaLysProLeuAspArg	260		PUBMED	
Db	2119	ACTTCACCTCTAGGCCAACAGTTAGTACCAAGGGAAACCTAAACGGCG	2178		REFERENCE	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Furuta,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramatsu,K., Hirakawa,T., Hirozane,T., Horii,F., Imorani,K., Itoh,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoch,H., Kawai,J., Koijini,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakaue,M., Sakaizumi,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomari,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Qy	261	LysLysValArgArgPheProGlyGluAlaLysProLeuAspArg	269		TITLE	Direct Submission
Db	2179	AGAAAAGTAGGGGGCCCTTCACCGA	2205		JOURNAL	Submitted (16-JUL-2001) to Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (Email: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
RESULT	2			COMMENT	CDNA library was prepared and sequenced in Mouse Genome	
AK032681				REFERENCE	Carninci,P. and Hayashizaki,Y.	
LOCUS				AUTHORS	High-efficiency full-length cDNA cloning	
DEFINITION				TITLE	Meth. Enzymol. 303, 19-44 (1999)	
SEQUENCE				JOURNAL		
VERSION				MEDLINE		
KEYWORDS				PUBMED		
SOURCE						
ORGANISM						
Mus musculus						
Mus musculus						
Mus musculus						
Mammalia; Eutheria; Rodentia; Sciurognath; Murinae; Mus						

二〇〇〇年

118-10-049-742-11.185

Encyclopedie Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken contributed to  
 Division of Experimental Animal Research in Riken.

Division of Experiments.  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:<http://Genome.gsc.riken.go.jp/>  
 URL:<http://Fantom.gsc.riken.go.jp/>

LOCATIONS/Qualifiers

SOURCE

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64 -2176 DOPAMINE RECEPTOR INTERACTING PROTEIN homolog  
 [Rattus norvegicus] (SPTR\_Q92G7, evidence: FASTY,  
 92.7%ID, 100%length, match=2109,  
 putative)  
 666 a 634 c 738 g 601 t

FEATURE

ENSE COUNT 1 - 2639

ALIGNMENT Scores:

Alignment No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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2	96.28%	93.31%	94.98%	11	0	0	0

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 b 21 AlaSerAspValGluLeuLysAlaTyrArgGlnLeuAlaValMetValHisProSP 40  
 1427 GCAATCGGACACTGAACTAAAGACGCCCTATAGGGAGCTAGCAGTAATGGTCCTGAT 14  
 b 41 LysAsnAlaIleSerProArgAlaGluGluAlaPheLysValLeuArgAlaAlaTrpAspIle 60  
 1487 AAAATACCATCCCCGGGTGAGGGCTTCAAAATATTGGCCAGCTTGAGCATTT 15  
 b 61 ValSerAsnAlaGluIleLysArgLysGluIleTyrGluMetLysGluAsnGluLeu 80  
 1547 GTCAAGAACCCGAGAGGGCAGGGATATGAGTAAGCTAACGGATGGCAAGAGATGAGCTC 16  
 b 81 SerArgSerValAsnGluPheLeuSerLysLeuGlnDaspAspIleLysGluAlaMetAsn 10  
 1607 AGCGGGTCAGGATAGGTTCTGTCGAACATPACAAGTGACTCAAGGGAACTGAC 16  
 b 101 ThreonineMetCysSerArgCysGlnGlyLysGluAsnArgLeuHisProArgGluPro 11  
 1667 ACCATGATGTTGCGCAAGATGGAGCTTGAAGCTAACGGCTAACAGTCATCTGTGAGAGACTTT 1  
 Qy 121 LysSerAlaArgTyrCysAlaGluCysAsnArgLeuHisProArgGluGlyLysAspPhe 1  
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 Db 141 TriAlaGluSerSerMetLeuGlyLeuLysIleIleTyrPheAlaLeuMetAspArgLys 1  
 1787 TGGCCAGAGTCGAGATGCTGGCTGGAGCTAACAGTCATCTGTGAGAGACTTT 1  
 Qy 161 ValIleTyrAspIleThrGluTyrGluTyrGluCysGlnArgValGlyIleSerProAspThrHis 1  
 Db 1847 GGTATGACATACAGGTGGCTGGAGCTAACAGTCATCTGTGAGAGACTTT 1

Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordheim, A., Marchionni, L., Mashima, H., Mazzarelli, J., Mombaerts, P., Nordheim, A., Ring, B., Ringwald, M., Rodriguez, J.I., Sakamoto, N., Saeki, H., Sato, K., Schonhöch, C., Seya, T., Shibata, Y., Storch, K.F., Suzui, Toyo-Oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wunshaw-Bois, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaka, and Hayashizaki, Y.	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES source	<p>Functional annotation of a full-length mouse cDNA collection</p> <p>Nature 409 (6821), 685-690 (2001)</p> <p>11217851</p> <p>5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I &amp; II Team.</p> <p>Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs</p> <p>Nature 420, 563-573 (2002)</p> <p>6 (bases 1-212)</p> <p>Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hasizume, W., Hayashida, K., Hayatsu, H., Hiramoto, N., Hirao, T., Hirozane, T., Hori, F., Imancani, K., Ishii, Y., Itoh, M., Kasawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, X., Nunazaki, R., Ohno, M., Ohsatani, T., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagaya, A., Takahashi, F., Takanuki-Akahira, Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.</p> <p>Direct Submission</p> <p>Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail: genome-rs@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed prepare mouse tissues</p> <p>Please visit our web site for further details.</p> <p>URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/</p> <p>COMMENT</p> <p>INTERACTING PROTEIN homolog [Rattus norvegicus] (SPTR) Q925G7, evidence: PASTY, 92.7% ID, 100% length, match=2109</p> <p>PUBTAXON</p> <p>Putative</p> <p>1. .2712</p> <p>/organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:B2:20120106" /db_xref="taxon:10090" /cl�="B23020106" /sex="male" /tissue_type="corpora quadrigemina" /clone_Tib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 177 - .2288</p> <p>/note="unnamed protein product; DOPAMINE RECEPTOR INTERACTING PROTEIN homolog [Rattus norvegicus]" (SPTR) Q925G7, evidence: PASTY, 92.7% ID, 100% length, match=2109</p> <p>CDS</p> <p>/codon_start=1 /protein_id=BAC32372.1" /db_xref="GI:26337373" /translation="MAQKHPGEERLGCAGHRSQGGTSLSSTGSSSYDPEILSFSGG TAPNGTREKKEHGPKTKTQPNNPAHSDSHGPGRGPGRGGYDDEETGG DOELSRNENETGYEDGSEPSFLSPSACMCGSCVPECTYSFGDGSSSLCLC ALJGDEELEYDEEPKPFPSRSVGGKKLISRGKHLFLLVGEYVETC PGRHLARKRSQDQDKRKGGLNVEEFLCQGQGFMWLLVGEYVETC CRKLKGSSLDLFRVWGVWARRLGWMMFQLSQSEFCVYGLIIRIVW</p>
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- Qy 21 AlaserAspValGluLeuLysLysAlaTyArgGlnLeuAlaValMetValHisProAsp 40  
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- Qy 41 LysAsHiShisProAlaGlaLugLjuAlaPheLeuArgAlaAlaLrrAspIle 60  
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- Qy 61 ValSerAsnAlaGluLysAspLysGluTYrgLumetLysArgMetAlaGluAsnGluLeu 80  
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- Qy 181 ArgValProTyrHistileSerPheGlySerArgIleProGlyThrArgGlyArgGlnArg 200  
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- Qy 221 ProProGlyGinMerProAsnGlyAsnPhePheAlaAlaProGlnProAlaProGlyAla 240  
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- Qy 261 LysLysValArgArgProPheGlnArg 269  
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AK045345 LOCUS 3022 bp mRNA linear HTC 05-DEC-2002  
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN  
full-length enriched library, clone:B23014C23 Product:DOPAMINE  
RECEPTOR INTERACTING PROTEIN homolog [Rattus norvegicus], full.  
insert sequence.  
ACCESSION AK045345  
VERSION GI:26337270  
KEYWORDS HTC; CAP Trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Etheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- REFERENCE AUTHORS Carninci,P., and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Medline  
MEDLINE 99219253  
PUBMED 10349636
- REFERENCE AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,C., Y., Muramatsu,M., and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 2049374  
PUBMED 11042159
- REFERENCE AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komio,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishimura,T., Harada,A., Yamamoto,R., Matsimoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Iwasa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kirz,A., and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20540913  
PUBMED 11076861
- REFERENCE AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamamoto,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehi,P., Lewis,S., Matuo,Y., Nakabido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bult,C., Brownstein,M.J., Celnici,P., de Bonalito,M.F., Gustincich,S., Hill,D., Fletcher,C., Fujita,M., Garboldi,M., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,D., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynnshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S., and Hayashizaki,Y.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
MEDLINE 21085660  
PUBMED 11217851
- REFERENCE AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
MEDLINE 11217852  
PUBMED 11217851
- REFERENCE AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashizaki,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Horii,P., Imotani,K., Ishii,Y., Itoh,M., Kasukawa,T., Kasukawa,T., Katoch,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Onsato,N., Okazaki,Y., Saito,R., Saito,H., Saka,K., Saka,S., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takada,F., Takeda,I., Takanishi,A., Muramatsu,M., and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute: 1-6-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 23-0045, Japan (E-mail: genome-resgsc.riken.go.jp., Tel: +81-45-503-9222,  
 Fax: +81-45-503-9216).  
 CDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 Please visit our web site for further details.  
[URL: http://genome.gsc.riken.go.jp/](http://genome.gsc.riken.go.jp/).

## COMMENT

Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 Please visit our web site for further details.

[URL: http://genome.gsc.riken.go.jp/](http://genome.gsc.riken.go.jp/)

FEATURES  
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 Location/Qualifiers

1. .3022  
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ORIGIN

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826 g

727 t

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 LOCUS  
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 ACCESSION  
 VERSION  
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 SOURCE  
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 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 Itoh, M.; Konno, H.; Okazaki, Y.; Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid-discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)

RESULT 6  
 AK083878  
 LOCUS  
 DEFINITION  
 AK083878 4053 bp mRNA linear HTC 05-DEC-2002  
 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length  
 interacting protein homolog (Rattus norvegicus), full insert  
 sequence.  
 AK083878  
 AK083878-1 GI:26101555  
 HTC; CAP trapper.  
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)

JOURNAL  
 Meth. Enzymol.  
 MEDLINE  
 99279233  
 10349656

REFERENCE  
 AUTHORS  
 Itoh, M.; Konno, H.; Okazaki, Y.; Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid-discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL  
 MEDLINE  
 20499374  
 11042159

REFERENCE  
 AUTHORS  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Meth. Enzymol. 303, 19-44 (1999)

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 20499374  
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REFERENCE  
 AUTHORS  
 Carninci, P., Aizawa, K., Nagaoaka, S., Sasasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kicsunai, T., Tashiro, H., Itoh, M.,

Db 1672 GTCAGCAACCCAGAGGGAGGAAGGAAACGGATGGCAGAGAATGGCTC 1681  
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 Db 121 LysSerAlaArgTyrosAlaGluCysAlaGluLysProAlaGluGluGlyAspPhe 140  
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 Qy 260 GlyLysLysValArgArgProProGlyGlnArg 269  
 Db 2222 GAAGAAAGTGGGGCCCCCTTCAGGA 2249

RESULT 6  
 AK083878  
 LOCUS  
 DEFINITION  
 AK083878 4053 bp mRNA linear HTC 05-DEC-2002  
 Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length  
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 MEDLINE  
 20499374  
 11042159

REFERENCE  
 AUTHORS  
 Carninci, P., Aizawa, K., Nagaoaka, S., Sasasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kicsunai, T., Tashiro, H., Itoh, M.,

Alignment Scores:  
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 Query Match: 94.07%  
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US-10-049-742-11 (1-269) x AK045345 (1-3022)

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ACCESSION	BUS3B214				Db	301	TGTAATAGGCTGATCCCTGCTGAGGAGACTTTEGGCACAGTCAGCATGTGAC	360
VERSION	BUS3B214.1	GT:22848655			Qy	149	LeuLysIleThrTyrPheAlaLeuMetAspGlyLysValtyAspIleThrGluPheAla	168
KEYWORDS	EST.				Db	361	CICAAAGATCACCCTACTTGCACTGACTGATGGAAAGGTGATGACATACAGGTGGCT	420
SOURCE	Homo sapiens (human)				Qy	169	GlyCysGlnArgValGlyIleSerProAspThrHisArgValProTyroHisIleSerPhe	188
ORGANISM	Homo sapiens				Db	421	GATGCCAGCGTGTAGGATCTCCAGATAACCACAGTCACATCACATCTCATT	480
COMMENT	Contact: Robert Straussberg, Ph.D. Email: cgabs@mail.nih.gov Tissue Procurement: ATCC				Qy	189	GlySerArgIleProGlyThrArgGlyArgGlnArgAlaThrProAspAlaProProAla	208
REFERENCE	1 (bases 1 to 942) http://mgc.ncbi.nih.gov/				Db	481	GGTTCTGGATTCCAGACCCAGGAGGAGGCCCCATGCCCCCTCTCTCT	540
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Qy	209	AspLeuGlnAspPhiLeuSerProAspThrHisArgValProProGlyInMetProAsnGly	228
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				Db	541	GATCTCAGGATTCTGAGTCGATCCCCAGGAGATGCCAATGG	600
JOURNAL	Unpublished				Qy	229	AsnPhePheAlaAlaProGlnProAlaProGlyAlaAlaAlaAlaLysProAsnSer	248
COMMENT	Contact: Robert Straussberg, Ph.D. Email: cgabs@mail.nih.gov Tissue Procurement: ATCC				Db	601	AACTCTTTGAGCTCTCAGCTGCCCTGAGCCGCTTAAGGCCAACG	660
CDNA Library Preparation:	Rubin Laboratory Consortium (LNL)				Qy	249	ThrValProLysGlyGluAlaLysProLysArgIleGlyLysValAlaArgPhePheGln	268
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium				Db	661	ACAGTACCCAAAGGAAAGCCAAACCTAACGCGGGAAAGTGTAGSAGGCCCTTC	720
DNA Sequencing by:	Agenourt Bioscience Corporation				Qy	269	Arg	269
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://Image.lnl.nih.gov/				Db	721	CGT	723
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Site 2: XhoI; cDNA made by oligo-dT priming.					AUTHORS	NIH-MGC http://mgc.nci.nih.gov/		
Directionally cloned into EcoRI/XhoI sites using the following 5' adapter: GGCACGAG(G).					TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
Library constructed by Liang Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).					JOURNAL	Unpublished		
Note: this is a NIH_MGC Library."					COMMENT	Contact: Robert Straussberg, Ph.D. Email: cgabs@mail.nih.gov		
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ORIGIN								
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Score:	1280.00	Matches: 239						
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DB:	13	Gaps: 0						
US-10-049-742-11 (1-269) x BUS3B214 (1-942)								
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Qy	49	GluAlaPhenLysValLeuArgAlaAlaTriaspSpIleValSerAsnAlaGluLysArgLys	68					
Db	61	GAGGCCCTCAAGGTTGCGAGCTGGCACATGTCAGCAATGTCAGGAAAGCAGAAG	120					
FEATURES	source							
	Location/Qualifiers							
	1..955							



98 AlaValAsnThrMetMetCysSerArgCysGlnGlyHisArgArgGluMetAsp 117  
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 Db 240 CGGGACCTTAAGATGCCGATACTGGCTGAGTGTAAATGGCTGAGTGAAGGA 299  
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Alignment Scores:  
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US-10-049-742-11 (1-269) x BU956189 (1-918)

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Qy 158 AspGlyLysValtryAspIleTerIleTrpIleGlyCysGlnArgValGlyIleSerPro 177  
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Qy 218 PheGlnValProProGlyGlnMetProAlaAlaProGlnProAla 237  
 Db 540 TTCAAGTAACTCCAGGGAGATGCCATGGGAACTTGTGAGTCCTGCC 599

Qy 238 ProGlyAlaAlaAlaAlaSerIleProAlaSerThrValProLysGlyGluAlaLysPro 257  
 Db 600 CCTGAGGCCGCTGAGCCCTAAAGCCACAGCAAGGAAAGGCCAAACCT 659

Qy 258 LysArgArgLysLysValArgArgPropheGlnArg 269  
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RESULT 10  
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 VERSION BU956189.1 GI:24185761  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1. (bases 1 to 918)  
 AUTHORS NIH-MGC http://mgc.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL3053 row f column: 18  
 High quality sequence stop: 544.  
 Location/Qualifiers 1..918  
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 /tissue\_type="adenocarcinoma, cell line"  
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 FEATURES source

Qy 227 AsnGlyAsnPheIleAlaAlaProGlyAlaAlaAlaSerIysPro 246  
 Db 543 AACGGAACTCTTGCAGCTCTCTGAGCTGCCCTGAGCCCTAAGGCC 602

Qy 247 AsnSerThrValProLyGlyGluAlaIysProlysArgArgLysLysValArgArgPro 266  
 Db 603 AACAGCACAGTACCCAAAGGAGAACCTTAAAGGGAGAGGAAATGAGGGGCC 662

Qy 267 PheGlnArg 269  
 Db 663 TTCCAACGT 671

Site 2: Xholi cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/Xhol sites using the following 5' adapter: GGCAAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.

BASE COUNT	234	a	228	C	238	g	- 218 t
ORIGIN							
Alignment Scores:							
Pred. No. :	3.93e-93						
Score:	1189.00						
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Best Local Similarity:	100.00%						
Query Match:	82.97%						
DB:	13						
Length:	918						
Matches:	223						
Conservative:	0						
Mismatches:	0						
Indels:	0						
Gaps:	0						

RESULT 11  
 BG763500 LOCUS 60235591P1 NIH\_MGC\_49 mRNA linear Homo sapiens cDNA clone IMAGE:4860694 5', mRNA sequence.

ACCESSION	BG763500	GI:	14074153	Qy	156	LeuMetaspGlyysValTyrAspIleThrGluTrpalaGlyCysGlnArgValGlyIle
KEYWORDS	BG763500..1	EST.		Db	302	CTGATGGATGGAAAGGTGATGACATCAGACTGGCTGGATCCAGTCACCGTGTAGTAC
SOURCE	Homo sapiens (human)			Qy	176	SePAspThrHisArgValProThrIleSerPheGlySerArgIleProGlyIhr
ORGANISM	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	362	TCCCCATATCCACAGTCCTCATCACATCTGGATTCTGGATTCAGGCACC
REFERENCE	1 (bases 1 to 878)			Qy	196	ArgGlyArgGlnArgAlaThrProAspAlaProProAlaAspPheLeuSer
AUTHORS	NIMH http://mrgc.nci.nih.gov/			Db	422	AGGGCGCGAGGCAACCCAGATCCCCTCTGGATTCAGTTCTGAGT
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			Qy	216	ArgIlePheGlnValProProGlyIleMetProAspGlyAsnPhePheAlaAlaPheGln
JOURNAL	Unpublished			Db	482	CGGATCTTCAGTACCCAGGCCATGCCAAATGGGAACCTTCAGCTCTGAGTCCTGAGTCAG
COMMENT	Contact: Robert.Straussberg, Ph.D. Email: cgapbs-r@mail.nih.gov			Qy	236	ProAlaProGlyAlaAlaAlaAlaLysProAlaSerThrValProLysGlyGluAla
	Tissue Procurement: ARCC/DCRP/DTTP			Db	542	CCTGGCCCTGGAGCCGCTGACCTTAAGCCCAAAGCACAGTACAGAACGGAGAACGCC
	cDNA Library Preparation: Ling Hong/Rubin Laboratory			Qy	256	LysProLysArgArgLysLysValAlaArgProPheGlnArg
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			Db	602	AAANCATAAGCGGGGGAGAAATGGAGAGGCCCTTCACAGT
	DNA Sequencing by: Incyte Genomics, Inc.					643
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov					
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	/tissue_type="melanotic melanoma, high MDR (cell line)"					
	/lab_host="DH10B (phage-resistant)"					
	/note="Organ: skin; Vector: pOTB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GGACGAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."					
	BASE COUNT	227 a	211 c	238 g	201 t	1 others
	ORIGIN					
	Alignment Scores:					
	Pred. No.:	9.83e-89	Length:	878		
	Score:	1138.00	Matches:	213		
	Percent Similarity:	99.53%	Conservative:	0		
	Best Local Similarity:	99.53%	Mismatches:	1		
	Query Match:	79.41%	Indels:	0		
	DB:	12	Gaps:	0		
	US-10-049-742-11 (1-269) × BG763500 (1-878)					
	Qy	56	AlaAlaTyrAspIleValSerIleSerIleAlaGluLysArgLysGlyGluMetIysArgMet	75		
	Db	2	GCAGCTGGAGCATTTGCAATGGCAAGGAGCTGATGAGTGAAGAACCAATG	61		
	Qy	76	AlaGluAsnGluLeuSerArgSerValAsnGluPheLeuSerLysLeuGlnAspPheIu	95		
	Db	62	GCAGAGATGAGCTGAGCCGGTAGAATAGATGCTGAAAGATGAGTGAAGAACCTC	121		
	Qy	96	LysGluAlaMetAsnThrMetMetCysSerArgCysGlnGlyLysBisArgArgPheGlu	115		
	Db	122	AAGGAGCCAAATGAATACTATGATGTTGAGCCATGCCAAAGGAAAGCATGGAGCTTGAA	181		
	Qy	116	MetAspArgGluProLysSerAlaArgTyrosAlaGluCysAsnArgLeuHisProAla	135		
	Db	182	ATGGACCGGGAACTTAAGGAGGCGCAATCTGCTGAGTATGGCTCATCTGCT	241		
	Qy	136	GluGluglyAsPPhetrPAlaGluSerSerMetLenglyLeuLysIleThrTyrPheAla	155		
	Db	242	GAGGAAGGAAACTTTRGGCAGAGTCAGCATGTTGGCTCAAGATCACCTACTTTGCA	301		
	BASE COUNT	219 a	244 c	239 g	202 t	
	ORIGIN					
	Alignment Scores:					
	Pred. No.:	1.01e-88	Length:	904		

Score:	1138.00	Matches:	215	DNA Sequencing by: Incyte Genomics, Inc.
Percent Similarity:	98.62%	Conservative:	0	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
Best Local Similarity:	98.52%	Mismatches:	2	Plate: LLNS614 row: 1 column: 03
Query Match:	79.41%	Indels:	1	High quality sequence stop: 643.
DB:	13	Gaps:	0	Location/Qualifies: 1. -723 2. organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone:"IMage:3867794" /tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 67" /note:Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."
US-10-049-742-11 (1-269) x BQ691177 (1-904)		FEATURES	BASE COUNT	
Qy	53 ValLeuArgGliaAlaLarphspIleValSerAsnAlaGluLysArgLysGluMet 72	Source	201 a	
Db	1 GTTTGCGAGCAGCTGGACATGTCAAAATGTAAGGAGTAGATGAGATG 60		208 g	
Qy	73 LysArgMetAlaGluAsnGluLeuSerArgSerValAsnGluPheLeuSerLysLeuGln 92		152 t	
Db	61 AAACGAATGGAGAATAGCTGAGCTTCTGCCAAAGCTGCCA 120			
Qy	93 AspAspLeuLysGluAlaMetCysSerArgCysGlnGlyLysHisArg 112			
Db	121 GATGACTCTAAGGGCCATGAAATACTAGTATGTTAGCGATGCCAAGGAAGCATAG 180			
Qy	113 ArgPheGluMetAspArgGluProLysserSerAlaArgTyrCysAlaGluCysAspArgLeu 132			
Db	181 AGGTTGAATGGACCTAACGAGTCCAGATACGTGTCAGTTAGGCTG 240			
Db	301 TACTTGCCACTGTGGATGAAAGTTGATGACATCACAGATGGCTGAGCTG 360	Alignment Scores:		
Qy	173 ValGlyIleSerProAspThrHisArgValProTyroHisIleSerPheGlySerArgIle 192	Pred. No.:	1.71e-83	
Db	361 GTAGGTATACTCCCAGATAACGATGCCCTATCACATCTCATTGTTCTCGGATT 420	Score:	1.07e-50	Length: 723
Qy	193 ProGlyThrArgGlyArgSerArgAlaLysProAspAlaproAspLysGlnAsp 212	Percent Similarity:	92.62%	Matches: 222
Db	421 CCAGCCACAGAGGGGGAGAGGCCACCCAGATGCCCTCTGCATCTTCAGGA 480	Best Local Similarity:	90.98%	Conservative: 4
Qy	213 PheLeuSerArgIlePheGlnValProGlyGlnMetProAsnGlyAsnPheHeAla 232	Query Match:	75.12%	Mismatches: 16
Db	481 TTCTGAGCTGGATCTTCAGTACCCCCAGGGAGATCCCCTATGGAACTCTTGA 540	DB:	10	Indels: 7
Qy	233 AlaProGlnProAlaProGlyAlaAlaAlaSerlysProAsnSerThrValProlys 252			Gaps: 2
Db	541 GCTCTCACCTGCCCTGCCCTGAGCCCTCTAACCCCAAAGCCAGAACCCAG 600			
Qy	253 GlyGluAlaLysProLysArgGlyLysValArgArg-ProPheGinArg 269			
Db	601 GGAGAACTAAACCTAACGAGGGCGSAACAAAGTGGGGCCCTTCACAGT 652			
RESULT 13				
LOCUS	B779250			
DEFINITION	6146514F1 NIH MGC_67 Homo sapiens cDNA clone IMAGE:3867794			
ACCESSION	BE779250			
VERSION	BE779250.1			
KEYWORDS	GI:10200448 EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 723)			
AUTHORS	NIH/MGC http://mgc.ncbi.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgs@psu@mail.nih.gov			
Tissue Procurement	ATCC			
cDNA Library Preparation	Life Technologies, Inc.			
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)			
Qy	223 GlyGlyMetProAsnGlyAsnPhePheAlaAlaProGlyAlaAlaAla 242			

Db	601	GGCGATGCCAAT-GGGAATTCTGGCAGTTCGCTGGAGCCCTG-	654	Db	71	GGTTTGCGACGTGGCATTCAGAAATGGTGAAGGAGGTATGAT	130
Qy	243	AlaSerLysProAsnSerThrValProLysGluAlaLysProLysGlyLys	262	Qy	72	tLysArgMetAlaGluAsnGluLeuSerArgSerValAsnGluPhoLeuSerLysLeuG1	92
Db	655	AGCTCTAACGAAAAGACATAA-CCCACGGAGAAAG-CAACCT--AACGGGGAAAAA	709	Db	131	GAAATCAAATGCGAGAAATGAGCTGAGCCGCTCAAGTGCA	190
Qy	263	ValArgArgPro	266	Qy	92	nAspAspLeuLysGluAlaMetAspThrMetMetCysSerArgCysGlnGlyLysIleSar	112
Db	710	GTGAGGAGGCC	721	Db	191	AGATGACTCTAGGGCAATGAAACTATGATGTTAGCCATGCAAGAAAGGATAG	250
RESULT	14			Qy	112	9ArgPheGluMetAspArgGluProLysSerAlaArgTyrCysAsnArgLe	132
BM424147	BN424147	BN424147	927 bp	mRNA	linear	EST 29-JAN-2002	
DEFINITION	ACENCOURT 6198639 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5517411	5', mRNA sequence.		Db	251	GAGGTGAAATGGACCGAACATAGTGCCAGATACTGTGCTGAGTSTAATTGGCT	310
ACCESSION	BM424147	EST.		Qy	132	uHispProAlaGluGluGlyLysAspPheTPalAgluSerSerMetLeuGlyLeuLysIle	152
VERSION	BN424147.1	GI:18392359		Db	311	GCATCTGGCTCAGGAGAACCTTGGGAGAGCTAGGATGAGCTACAGTAGCAG	370
KEYWORDS	Homo sapiens (human)			Qy	152	rTyrPheAlaLeuMetAspGlyLysValtyAspIleThrClutPheGlyLysGlnAr	172
SOURCE	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Batheria; Primates; Catarrhini; Hominidae; Homo.		Db	371	CTACPTGACTGATGATGAGCTGATGACATCACAGTGCAGTCAG	430
REFERENCE	1 (bases 1 to 927)			Qy	172	qValGlyLysSerProAspPheThiGlyValProTyAspIleThrClutPheGlyLysGlnAr	192
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			Db	431	TGTAGCTATCTCCCAAGATACCACAGAGTGCCTCPATCACATCTCATTTGTTCTGGAT	490
TITLE	Mammalian Gene Collection (MGC)			Qy	192	eProGlyThrArgGlyArgGlnArgAlaThrProAspAlaProProAlaAspLeuGlnAs	212
JOURNAL	Unpublished			Db	491	TCCAGGCCACAGGCGAGGAGGAGGCCACCCCCAGATGCCCTCCCTGCTGATCTAGGA	550
COMMENT	Contact: Robert Straubberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: DOD/DRP CDNA Library Preparation: Rubin Laboratory			Qy	212	pTyrPheAlaLeuMetAspGlyLysValtyAspIleThrClutPheGlyLysGlnAr	232
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			Db	551	TTTCCTGAGTCGGATTTCAAGTACCCCAAGGGAGATGCCCATGGGAACTTCTTG	610
AUTHORS	Title: Mammalian Gene Collection (MGC)			Qy	232	IaAla-ProGlnProAla-ProGlyAlaAlaAlaAlaSer---LysProAlaSerThrVa	250
TITLE	Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			Db	611	CAGTCCTCAACCTGCCCCCTGGAGCCCCCTGCAAGGCCAGT	670
JOURNAL	Place: LLCMW019 row: j column: 04			Qy	250	1ProLysGlyGluAlaLysProLys	258
COMMENT	High quality sequence stop: 460			Db	671	ACCCCAAGGGAG--AAACCCAA	692
FEATURES	Location/Qualifiers			RESULT	15		
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	/note="Organ: Skin; Vector: pOTB1; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH_MGC Library."			ORGANISM			
BASE COUNT	236 a	241 c	245 g	REFERENCE			
ORIGIN	204 t	1 others		AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>		
Alignment Scores:				TITLE	Mammalian Gene Collection (MGC)		
Pred. No.:				JOURNAL	Unpublished		
Score:	2.44e-83	Lengt		COMMENT	Contact: Robert Straubberg, Ph.D.		
Percent Similarity:	1076.00	Matches:	927	Email: cgaps-r@mail.nih.gov			
Best Local Similarity:	93.51%	Conservative:	214	Tissue Procurement: CLONETECH Laboratories, Inc.			
Query Match:	92.64%	Mismatches:	2	CDNA Library Preparation: CLONETECH Laboratories, Inc.			
DB:	75.09%	Indels:	6	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)			
		Gaps:	2	DNA Sequencing by: Incyte Genomics, Inc.			
US-10-049-742-11 (1-269) x BM424147 (1-927)				Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			
Qy	33	LeuAlaValMetVal-HisProAspLysAsnHisHisProArgAlaGluAlaPheH	52	Plate: LCM1145 row: k column: 23			
Db	11	CTGGCAGTGTGGTNCATCTGACAAATTCACTCCGGCTGAGGGCTTCA	70	High quality sequence stop: 697.			
Qy	52	svalleuArgAlaAlaLysProAspIleValSerAsnAlaGluLysArgLysGluTyrGluMe	72	Location/Qualifiers			
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Search completed: December 1, 2003, 12:06:03  
 Job time : 2552 secs

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BASE COUNT	201	a	207	c	272	g	194	t
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Site 1: SFI I (ggcgctggcc); Site 2: SFI I (ggccatggcc
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adaptor sequence: 5'-CACGCCATTATGCC-3'; and 3' adaptor
sequence: 5'-ATTCTAGGGCGAGGCCACATG-dT(30)BN-3';
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Db	2	AGAAATGTAAAGCAAGGGAAGGTATGAGAATGAAATGCAAGATAAGTCAG	61				
Qy	82	ArgSerValAsnGluPheLeuSerLysLeuGinAspAspLeuLysGluAlaMetAsnThr	101				
Db	62	CGCTCAGTAATGAGTTCTGTCCAAGTGCAAGATGACTCAAGGCCAATGAAATTCT	121				
Qy	102	MetMetCysSerArgCysGlnGlyLysHi sArgArgPheGluMetAspArgGluProLys	121				
Db	122	ATGATGTAGCCGATGCCAAGGAAAGCATAGGAGTTGAATGGCCGGAACCTTAAG	181				
Qy	122	SerAlaArgTyrcysAlaGluCysAsnArgLeuHisProAlaGluGluGlyAspPheTrp	141				
Db	182	AGGCCAGATACATGTGTGAGCTAAAGCCTGCATCTGCTAGGAGGAGCTT-TGG	240				
Qy	142	AlaGluUserSerMetLeuGlyLeuLysIleThrTyrPheAlaLeuMetAspGlyLysIva	161				
Db	241	GCAGAGTCAAAGCATGTTGGCTCTCAAGATCACCTACCTTGCACTGATGGAAAGGTG	300				
Qy	162	TyrAspIleThrGlutPheAlaGlyCysGlnArgValGlyIleSerProAspThrHisArg	181				
Db	301	TATGACATACAGATGGCTGATGCCAGCTCTCCAGATACCCAGATAACCAAGAGA	360				
Qy	182	ValProTyRHisIleSerPheGlySerArgIleProGlyThrArgGlyArgGlnArgAla	201				
Db	361	GTCCTCTATCACATCTCATTCATTCATGATTCGATTCAGGATTCAGGAACTTCAAGTACCC	420				
Qy	202	TheProAspAlaProProAlaAspLeuGlnAspPheLeuSerArgIlePheGlnValPro	221				
Db	421	ACCCAGATGCCCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG	480				
Qy	242	AlaAlaSerLysProAsnSerThrVal_ProLysGlyGluAlaLysProLysArgArgLY	261				
Db	541	GGAGCTTAACGCCAAACAGTCTCCATGGGAAGCAAACCTCAGGGCAACCTCAGGGCCGAA	600				
Qy	261	SlySvalArgGlyProPhe	267				
Db	601	GAAAGTGAGGAGGCCCTTC	619				